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Thanks,
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:36:31 ; Search time 36 Seconds
(without alignments)
2415.330 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSCSGLSRVLVAVATLV.....KPGFLASVLPVDRRPGAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2275	100.0	422	Q16542	Q16542 homo sapien
2	1897	83.4	432	Q64385	Q64385 mus musculus
3	1871	82.2	432	P70225	P70225 mus musculus
4	1860.5	81.8	431	Q99MF4	Q99MF4 rattus norv
5	391	17.2	372	Q88507	Q88507 mus musculus
6	269	11.8	228	Q35228	Q35228 mus musculus
7	259.5	11.4	229	Q75269	Q75269 homo sapien
8	255.5	11.2	229	Q14213	Q14213 homo sapien
9	215.5	9.5	881	Q57519	Q57519 xenopus lae
10	211.5	9.3	422	Q75462	Q75462 homo sapien
11	210.5	9.3	422	Q9UHH5	Q9UHH5 homo sapien
12	209.5	9.2	425	Q9JMS8	Q9JMS8 mus musculus
13	192	8.4	227	Q9GLW3	Q9GLW3 ursus marit
14	191	8.4	327	Q9ET05	Q9ET05 marmota mon
15	190.5	8.4	206	Q16354	Q16354 homo sapien
16	190.5	8.4	268	Q8TD78	Q8TD78 homo sapien

17	189.5	8.3	611	13	Q9PTH9	Q9PTH9 xenopus lae
18	189	8.3	288	4	Q96P36	Q96P36 homo sapien
19	189	8.3	349	4	Q9UJ35	Q9UJ35 homo sapien
20	189	8.3	376	4	Q96P35	Q96P35 homo sapien
21	187.5	8.2	327	11	Q91ZK7	Q91ZK7 sigmodon hi
22	187.5	8.2	625	6	Q9XS92	Q9XS92 trichosurus
23	187.5	8.2	626	13	Q90WG7	Q90WG7 cynops pyrr
24	185.5	8.2	611	13	Q9IBF6	Q9IBF6 xenopus lae
25	185.5	8.2	611	13	Q9PTI0	Q9PTI0 xenopus lae
26	185	8.1	346	13	Q93404	Q93404 oreochromis
27	183	8.0	622	6	Q9N0J7	Q9N0J7 callithrix
28	181.5	8.0	636	13	Q90Z16	Q90Z16 paralichthy
29	179.5	7.9	538	13	Q9DFU0	Q9DFU0 sparus aura
30	174.5	7.7	1280	13	Q90933	Q90933 gallus gall
31	174	7.6	608	11	Q99J21	Q99J21 mus musculu
32	172	7.6	638	13	Q9DE08	Q9DE08 oncorhynch
33	161.5	7.1	918	13	Q9W6U9	Q9W6U9 gallus gall
34	159.5	7.0	173	13	Q8QFL5	Q8QFL5 brachydanio
35	156.5	6.9	198	6	O18985	O18985 cervus elap
36	155.5	6.8	1419	13	Q98SW3	Q98SW3 brachydanio
37	153.5	6.7	600	13	Q9PTP0	Q9PTP0 carassius a
38	152.5	6.7	217	6	O46386	O46386 mustela vis
39	152	6.7	604	13	Q8QG54	Q8QG54 cyprinus ca
40	150	6.6	1032	13	Q8UVD6	Q8UVD6 brachydanio
41	149.5	6.6	332	11	Q924V5	Q924V5 cavia porce
42	148.5	6.5	1389	13	Q90Z69	Q90Z69 brachydanio
43	147	6.5	1256	11	Q925S5	Q925S5 mus musculu
44	146.5	6.4	861	6	Q9BEG2	Q9BEG2 bos taurus
45	146	6.4	335	11	Q9QUW1	Q9QUW1 mus musculu

ALIGNMENTS

RESULT 1

Q16542 PRELIMINARY; PRT; 422 AA.
ID Q16542 Q14626;
AC Q16542; Q14626;
DC Q1-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Interleukin-11 receptor (Interleukin 11 receptor, alpha).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RX MEDLINE=95399754; PubMed=7670098;
RA Cherel M., Sorel M., Lebeau B., Dubois S., Moreau J.F., Bataille R.,
RA Minvielle S., Jacques Y.;
RT "Molecular cloning of two isoforms of a receptor for the human
RT hematopoietic cytokine interleukin-11.";
RL Blood 86:2534-2540(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Van Leuven F., Stas L., Hilliker C., Miyake Y., Gossler A.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3-390 FROM N.A.
RC TISSUE=PLACENTA;
RA Cherel M., Sorel M., Dubois S., Lebeau B., Moreau J., Jacques Y.,
RA Minvielle S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32324; AAB36492.1; -;
DR EMBL; U32324; AAB36492.1; -;
DR EMBL; U32323; AAB36491.1; -;
DR EMBL; U32323; AAB36491.1; -;

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DR EMBL; Z46595; CAA86570.1; -.
DR EMBL; BC003110; AA031110.1; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003599; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 422 AA; 45222 MW; 1F8BC05C139FC326 CRC64;

Query Match 100.0%; Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9e-167;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
DB 1 MSSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCCPGVTAGDPVSWF 60

QY 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSC 120
DB 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSC 120

QY 121 QAADYENFSCWSPQSISGLTRYLTSYRKTKTVLGADSORSPSTGMPCCQDPLGAARC 180
DB 121 QAADYENFSCWSPQSISGLTRYLTSYRKTKTVLGADSORSPSTGMPCCQDPLGAARC 180

QY 181 VVHGAEFWSQYRINVTEYNPLGASTRLDVSLSQTLRPDPQGLRVESVPGYPRRLRASW 240
DB 181 VVHGAEFWSQYRINVTEYNPLGASTRLDVSLSQTLRPDPQGLRVESVPGYPRRLRASW 240

QY 241 TYPASWPCQPHFLKFLRYRPAQHPAMSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
DB 241 TYPASWPCQPHFLKFLRYRPAQHPAMSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300

QY 301 AGTWSTWSPWAMGTPSTGTIPKEIPAWGOLHTQPEVQVDSAPPSPRPSLQPHRLLDHR 360
DB 301 AGTWSTWSPWAMGTPSTGTIPKEIPAWGOLHTQPEVQVDSAPPSPRPSLQPHRLLDHR 360

QY 361 DSVEQVAVLASGLISFLGLVAGALALGLWLRRLRGKDGSKPKCFGLASVIPVDRRFGAP 420
DB 361 DSVEQVAVLASGLISFLGLVAGALALGLWLRRLRGKDGSKPKCFGLASVIPVDRRFGAP 420

QY 421 NL 422
DB 421 NL 422

RESULT 2
Q64385 ID Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin-11 receptor ALPHA chain 1 precursor (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAL OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=95045367; PubMed=7957045;
RA Hilton D.J., Hilton A.A., Raicevic A., Rakar S., Harrison-Smith M.,
RA Gough N.M., Begley C.G., Metcalf D., Nicola N.A., Willson T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
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RT for high affinity binding and signal transduction."
RN EMBO J. 13:4765-4775(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA Neuhaus H., Bettenhausen B., Bilinski P., Simon-Chazottes D.,
RA Guenet J.L., Gossler A.;
RL Dev. Biol. 166:521-542(1994).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6;
RA Gossler A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97129000; PubMed=8973540;
RA Bilinski P., Hall M.A., Neuhaus H., Gissel C., Heath J.K., Gossler A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RL mouse genome."
[5]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
DR EMBL; X74953; CAA52908.1; -.
DR EMBL; U14412; AAA53248.1; -.
DR EMBL; X94162; CAA63873.1; -.
DR EMBL; X94163; CAA63873.1; JOINED.
DR EMBL; BC004619; AA04619.1; -.
DR HSP; P16471; Ibp3.
DR HGD; MGI-107426; Il11ral.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 432 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1.
FT DOMAIN 24 367 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 368 393 POTENTIAL.
FT DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 41 102 IG-LIKE C2-TYPE DOMAIN.
FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 432 AA; 46655 MW; 068389943502BBFC CRC64;

Query Match 83.4%; Score 1897; DB 11; Length 432;
Best Local Similarity 83.5%; Pred. No. 1e-137;
Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
DB 1 MSSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCCPGVTAGDPVSWF 60

QY 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSC 120
DB 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSC 120

QY 121 QAADYENFSCWSPQSISGLTRYLTSYRKTKTVLGADSORSPSTGMPCCQDPLGAARC 180
DB 121 QAADYENFSCWSPQSISGLTRYLTSYRKTKTVLGADSORSPSTGMPCCQDPLGAARC 180
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OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Li R., Hartley L., Robb L.;
 RT "Expression of interleukin-11 and interleukin-11 receptor alpha chain
 in the rat uterus in the peri-implantation period.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF347936; AAK29624.1;
 DR HSSP: P16471; 1BP3
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003530; Hemtopoptn_L_F3.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; FN3; 2.
 DR SMART: SM00410; IG_Like; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 431 AA; 46784 MW; E086FD6B1688180B CRC64;
 Query Match 81.8%; Score 1860.5; DB 11; Length 431;
 Best Local Similarity 82.0%; Pred. No. 6.3e-135;
 Matches 347; Conservative 21; Mismatches 54; Indels 1; Gaps 1;
 QY 1 MSSCSGLSLRVAVATALVSASSPCQAWPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MSSRSGLTRVLAVATALVSSSTPCQAWPGVQYQGPGRVPMCLCCPGVNAAGTPVSWF 60
 QY 61 RDGPKLLQPDGSLGHELVLAQADSTDEGTYICQLDGLAGLGTVLQLYPPARPVSC 120
 DB 61 RDGDSRLQPDGSLGHELVLAQADSTDEGTYICQLDGLAGLGTVLQLYPPARPVSC 120
 QY 121 QAADYENFSCWTSPQISGLPTRYLTSYRKTKVLGADSRQSPSTGPPCPQDPLGAARC 180
 DB 121 QAVDYENFSCWTSPQISGLPTRYLTSYRKTKVLGADSRQSPSTGPPCPQDPLGAARC 180
 QY 181 VVHGAEPWSYRINVTENVPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASW 240
 DB 181 VVHGAEPWSYRINVTENVPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRRLHASW 240
 QY 241 TYPASWPCQPHLLKFLQYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVASRDFLD 300
 DB 241 TYPASWRRQPHLLKFLQYRPAQHPAWSTVEPIGLEELITDVAAGLPHAVRVASRDFLD 300
 QY 301 AGTWSTWSPAWGTPSTGTIPKPAWQLHTQP-EVEPOVDSPPAPRPSLQPHRLLDH 359
 DB 301 AGTWSAWSPEAWGTPSTGTIPKPAWQLHTQP-EVEPOVDSPPAPRPSLQPHRLDH 360
 QY 360 RDSVQVAVLASIGLISFLGLAGALALGWLRLRGKDGSPKPGFLASVIVDRRPGA 419
 DB 361 RDPLEQVAVLASIGLISFLGLAVGALALGWLRLRRSGKDGKPGFLADMPIDKLPGI 420
 QY 420 PNL 422
 DB 421 PNL 423
 RESULT 5
 O88507 PRELIMINARY; PRT; 372 AA.
 AC O88507;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ciliary neurotrophic factor receptor alpha precursor.
 GN CNTRF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RA Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Maeda M., Yaguchi N., Hanyuu C., Nakata Y., Onoda N., Tulin E.E.,
 RA Kojima T., Hasegawa M., Kikuchi Y., Nomura H.;
 RT "Mouse homolog of human ciliary neurotrophic factor receptor.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF068615; AAC25711.1;
 DR MGD; MGI:99605; Cntrf.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003530; Hemtopoptn_L_F3.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
 KW Immunoglobulin domain; Receptor; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT ALPHA.
 SQ SEQUENCE 372 AA; 40831 MW; EB75A9EE6A1BB8C8 CRC64;
 Query Match 17.2%; Score 391; DB 11; Length 372;
 Best Local Similarity 31.8%; Pred. No. 3.9e-22;
 Matches 113; Conservative 49; Mismatches 163; Indels 30; Gaps 12;
 QY 1 MSSCSGLSLRVAVATALVSASSPCQAWPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MTASVFWACAVLAATAAAVYTKHSPQE--APHVQYERLGAADVTLPCGTASWDAAVTWR 58
 QY 61 RDGPKLLQPDGSLGHELVLAQADSTDEGTYICQLDGL-ALGTTVTQLQYGPAPRVVS 119
 DB 59 VNGCTD--LAPDLLGSQLILSLGSLYACFHRDSWHLRHQLLVGLPPREPVL 115
 QY 120 QCAADY-ENFSCWTSPQISGLPT-RYLTSYRKTKVLGADSRQSPSTGPPCPQDPLGA 177
 DB 116 CRSTNYPKGYCSWH-----LPTTYIPNTFNVTNLHGSK-----IMVCEKDPALK 161
 QY 178 ARCWHGAEPWS--QYRINVTENVPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRR 235
 DB 162 NRCHIRYMLFSIKYKVSISVSNALGHNTATTFDEFTIVKDPDENVAVRPSNPRR 221
 QY 236 LRASWTYPASWPCQPHLLKFLQYRPAQHPAWSTVEPA-GLEEVITDVAAGLPHAVRV 294
 DB 222 LEVTWQTPSTWPDSPESFPLKFFLRYRPLLDQWQHVLSGDTAHTTIDAYAGKEYIIQVA 281
 QY 295 ARDFLDAGTWSTWSPAWGTPSTGTIPKPAWQLHTQPEVQVDSPPAPRPS 349
 DB 282 AKD-NEIGTWSWDSVAHAATPTEE-PRHLTTEAQ---APETTTSTTSSLAPPPT 331
 RESULT 6
 O35228 PRELIMINARY; PRT; 228 AA.
 AC O35228;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cytokine receptor-like molecule (Epstein-Barr virus induced gene
 3).
 GN EB13 OR EB13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,

Db 66 YR- ---LGMARGHS- ---WPCLOQTPTSTCTITDQVLFSEMAPYVLNVTAHVFWGSS 116
QY 206 RLDDVSLQSLRPPGLOGLRVESVPGVPRRLRASWTVPASWPCPHFLKLFKLOVRAQH 265
Db 117 SFVFPTEHILRPPDPEGRVLS- ---PLAERHVQVQWVEPPGSPFFFEISLKYWIRKQGA 174
QY 266 PAWSTVEPAGLEEYITDAVAGLPHA- ---VRYSDARDFDAGTWTWSPSEAMGTPTSG 318
Db 175 ARPHRVGPTEATSFILRAVR- ---PRARYVQVAAQDLTDYGLSDWLSLPATATMSLG 228

RESULT 9

057519 PRELIMINARY; PRT; 881 AA.
AC 057519;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Gp130p1.
DE Cytokine-like factor-1 precursor.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RT "Partial characterization of putative Xenopus gpl30.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -;
DR HSSP; P40189; IBOU.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hemtopopn_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D2D1138A0 CRC64;

Query Match 9.5%; Score 215.5; DB 13; Length 881;
Best Local Similarity 23.3%; Pred. No. 3.3e-08;
Matches 88; Conservative 61; Mismatches 145; Indels 83; Gaps 19;

QY 1 MSSCSGLSRVLVAVATALVYASSPCPQAWGPGVQVGPGRSVKLCPCGVTA- ---GDP 56
Db 5 ISFCLISSVVLIVHQELVKV- ---CGRIFFDPCIVHGERPFTA-YCVINOTCLUREDASR 60
QY 57 VSWFRDG- ---BPKLQGPDSGLGHVLAQADSTDEGTICQTL-DGALGT- ---VT 106
Db 61 IYWLKGVKVPETQYEILNQTTSVTENL- ---TTLSPLTCNVASGHVANTLYGIF 115
QY 107 LQGLYPPARVY-VSCQAADYENFSCWSPSQISGLPTRYITSYRKTKTVLGADSORRSPST 165
Db 116 FTGLGPDKPTNLTCIVYNODNLTCITDWPGRPTNLPTNTLSHR-WAHFGANYCRGANS 174
QY 166 GPWPCPDPLGAARCVH- ---GAEPWSOYRINVTENVPLG-ASTLLDVSLOSILRPDPQ 222
Db 175 - ---CTHSPGFQYIITTCQVEATNEIGIKSTLTIDPVNIVKPNPQ 220
QY 223 GLRVESVPGVPRRLRASWTVPASWPCPHFLKLFKLOVRAQHAWSTV- ---EP 273
Db 221 LSELISLELPNALKIEKNPIT- ---NAENLKNYIRYRPVKTDWEMVPEEDTASHRDS 276
QY 274 AGLEEVITDAVAGLPHAVRSARDFLDAGTWTWSPSEAMGTPTSGTIPKEIPA 326
Db 277 FTLODLLPNTYEV- ---SIRCIHKD- ---GHGFWSWSELKQVTPDEA- ---PPSRG- --- 322
QY 327 WQLHTOPEVEPOVDSP 343
Db 323 - ---PDIWKKIDSP 332

RESULT 10

075462 PRELIMINARY; PRT; 422 AA.
AC 075462;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytokine-like factor-1 precursor.
GN CLF-1.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-I Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hemopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059293; AAC28335.1; -;
DR EMBL; AF073515; AAD39681.1; -;
DR HSSP; PF6471; IBP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR Receptor; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFB01B84228 CRC64;

Query Match 9.3%; Score 211.5; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 2.7e-08;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

QY 7 GLSRVLVAVATALVYASSPCPQAWGPGVQVGPGRSVKLC- ---PGVTAGDPVSWF 60
Db 30 GAPRAGSGAHTAVISPODPTILLI- ---GSSLATCSVHGDPGATA-EGLYWT 77
QY 61 RDGE- ---PKLQGPDSGLGHVLAQAD- ---STDEGTICOTLDGALGTVTQLGY 112
Db 78 LNGRRLPELSRVNLAS- ---TLALANLNGSRQSRGDLNVLCHARDGSIAGSLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWSPSQ- ---ISGLPTRYITSYRKTKTVLGADSORRSPSTGWP 169
Db 135 PERPVNTSCWSKNMKDLTCRWTPGAHGETLHTNYSKYLRWYQDNTCEEYHTVGPHS 194
QY 170 C- ---PODPLGAARCVHGAEPWSOYRINVTENVPLG-ASTLLDVSLOSILRPDPQGLRV 226
Db 195 CHIPKD- ---LALFTPEIWEATNRLGARSVDVLILDVTTDPPDVHV 243
QY 227 ESVPGYPRRLRASWTVPASWPCPHFL- ---KFRLOYRPAQHAWSTVEP- ---AG 275
Db 244 SRVGLEDQLSVRWSP- ---PALKDFLFQAKYQIRYVEDSDVKVDDVSNQTSCLRAG 300
QY 276 LEEVITDAVAGLPHAVRSARDF- ---LDAGTWTWSP-PEA- --- 311
Db 301 LK- ---PCTYVYQVRCNPFGIYKSKAGIWSHPTAASTPRSRPGPGGACEP 353
QY 312 -WGTPTSTGTIPKEIP- ---AWGQLH 331
Db 354 RGCEPSSGPVRRELKQFLGWLKH 377

RESULT 11

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Q9UHH5
ID Q9UHH5 PRELIMINARY; PRT; 422 AA.
AC Q9UHH5;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Class I cytokine receptor.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmsberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSSP; PI6471; IBP3.
DR InterPro; IPR002996; CR1A.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 9.3%; Score 210.5; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 3.3e-08;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

QY 7 GLSRVLVAVATLVSSSPCPQAWGPPGVQYQPGRSVKLCC-----PGVTAGDPVSWF 60
DB 30 GAPRAGSGAHTAVISQDPPTLLI-----GSSLATCSVHGDPGATA-EGLYWT 77
QY 61 RDGE---PKLQGPDSGLGHELVLAQD-----STDEGTYICQTLGALGGTVTLQGY 112
DB 78 LNGRRLPELSVLNAS---TLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 134
QY 113 PARPV-VSCQAADYENFCTWSPSQ--ISGLPTRYLTYSRKKTVLGADSORRSPSTGWP 169
DB 135 PEKPNVNSCWNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEEYHVGPHS 194
QY 170 C--PODPLGARCVCVHGAETFSQYRINTVEVNPGLG-ASTRLDVSLSQILRPPDPOGLRV 226
DB 195 CHIPKD-----LALFTPEIWEATNRLGARSVDLTLDVLTDPDPPEVHV 243
QY 227 ESVGYPRLRASWTYPASWPCQPHLL--KFLQYRPAQHPAWSTVEP-----AG 275
DB 244 SRVGLEQLSVRWVSP---PALKDFLQAKYQIRYVEDSDVKVDDVSNQTSCLAG 300
QY 276 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWSTWS-PEA----- 311
DB 301 LK-----PGTVFYVQRCNPGIYGSKKAGIWEWSHPTAASPRSERPCGGGACEP 353
QY 312 -WGTPSTGTIPKEIP---AWGQLH 331
DB 354 RGGEPSGPGVRRELKQFLGWLKKH 377

RESULT 12
Q9JMS8
ID Q9JMS8 PRELIMINARY; PRT; 425 AA.
AC Q9JMS8;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Cytokine receptor like molecule 3 precursor.
GN CRLF1 OR CRLF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
RT "cytokine receptor like molecule 3.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040038; BAA92777.1; -.
DR HSSP; PI6471; IBP3.
DR MGD; MGI:1340030; Cr1f1.
DR InterPro; IPR002996; CR1A.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Receptor; Signal.
FT SIGNAL 1 34 POTENTIAL.
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 9.2%; Score 209.5; DB 11; Length 425;
Best Local Similarity 23.9%; Pred. No. 3.9e-08;
Matches 89; Conservative 53; Mismatches 138; Indels 93; Gaps 18;

QY 17 TALVSASSPCQAWGPPGVQYQPGRSVKLCC-----PGVTAGDPVSWFRDGEKLLQG 70
DB 43 TAVISQDPPTLLI-----GSSLQATCSIHCDTPGATA-EGLYWTNG--RRLPS 88
QY 71 PDSGLGHELVLAQADSTDEGT-----YICQTLGALGGTVTLQGYPPARPV-VSCQA 122
DB 89 ELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPFNISCWS 148
QY 123 ADYENFCTWSPSQ--ISGLPTRYLTYSRKKTVLGADSORRSPSTGWPWC--PODPLGNA 178
DB 149 RNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEEYHVGPHSCHLIPKD----- 203
QY 179 RCVHGAETFSQYRINTVEVNPGLG-ASTRLDVSLSQILRPPDPOGLRVESVPGYPRRLR 237
DB 204 -----LALFTPEIWEATNRLGARSVDLTLDVLTDPDPDVHVSRRVGGLEDQLS 257
QY 238 ASWTYPASWPCQPHLL--KFLQYRPAQHPAWSTVEP-----AGLEEVIITDAVAG 286
DB 258 VRWVSP---PALKDFLQAKYQIRYVEDSDVKVDDVSNQTSCLAGLK-----PG 307
QY 287 LPHAVRVSARDP-----LDAGTWSTWS-PEA-----WGTPSTGTIP 321
DB 308 TVIFYVQRCNPGIYGSKKAGIWEWSHPTAASPRSERPCGGVCEPRGEGSSGPVR 367
QY 322 KEIP---AWGQLH 331
DB 368 RELKQFLGWLKKH 380

RESULT 13
Q9GLW3
ID Q9GLW3 PRELIMINARY; PRT; 227 AA.
AC Q9GLW3;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Prolactin receptor (Fragment).
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20086658; PubMed=10618652;
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;
RT "Cloning and sequence analysis of the extracellular region of the
RT polar bear (Ursus maritimus) luteinizing hormone receptor (LHR),
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor
RT (PLR) genes and their expression in the testis of the black bear
RT (Ursus americanus)".
RL Mol. Reprod. Dev. 55:136-145(2000).
DR EMBL; AF169792; AAG10648.1; -.
DR HSSP; PI4787; IAN3.
```

[illegible]

Sat Jan 18 21:53:46 2003

us-09-924-338-2.rspt

Page 9

Search completed: January 17, 2003, 19:39:09
Job time : 45 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:35:38 ; Search time 14 Seconds
(without alignments)
1250.215 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSLSLVLNAVATLV.....KPGFLASVIPVDRRPGAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	395.5	17.4	460	1 IL6A_MOUSE	P22272 mus musculus
2	392	17.2	372	1 CNTR_RAT	Q08406 rattus norv
3	390.5	17.2	462	1 IL6A_RAT	P22273 rattus norv
4	382	16.8	372	1 CNTR_HUMAN	P26992 homo sapien
5	381	16.7	362	1 CNTR_CHICK	P51641 gallus gall
6	360	15.8	468	1 IL6A_HUMAN	P08887 homo sapien
7	326.5	14.4	467	1 IL6A_PIG	O18796 sus scrofa
8	234	10.3	831	1 PRLR_MELGA	Q91094 meleagris g
9	221	9.7	830	1 PRLR_COLLI	Q90374 columba liv
10	214	9.4	831	1 PRLR_CHICK	O04594 gallus gall
11	209.5	9.2	581	1 PRLR_SHEEP	O46561 ovis aries
12	204.5	9.0	581	1 PRLR_BOVIN	Q28172 bos taurus
13	204	9.0	616	1 PRLR_RABIT	P14787 oryctolagus
14	197.5	8.7	581	1 PRLR_CEREL	Q28235 cervus elap
15	190	8.4	327	1 IL2B_MARMO	Q61729 marmota mon
16	190	8.4	327	1 IL2B_SHEEP	O02815 ovis aries
17	189	8.3	622	1 PRLR_HUMAN	P16471 homo sapien
18	186	8.2	1266	1 NCBA_CHICK	Q03696 gallus gall
19	184	8.1	327	1 IL2B_BOVIN	P46282 bos taurus
20	183	8.0	327	1 IL2B_CEREL	Q28234 cervus elap
21	183	8.0	610	1 PRLR_RAT	P05710 rattus norv
22	174.5	7.7	324	1 IL2B_PIG	Q28938 sus scrofa
23	174.5	7.7	329	1 IL2B_FELCA	O02744 felis silve
24	174	7.6	608	1 PRLR_MOUSE	Q08501 mus musculus
25	173.5	7.6	630	1 PRLR_ORENI	Q91513 oreochromis
26	167.5	7.4	328	1 IL2B_HUMAN	P29460 homo sapien
27	166.5	7.3	761	1 NCA2_HUMAN	P13592 homo sapien
28	164.5	7.2	328	1 IL2B_MACMU	P48095 macaca mula
29	164	7.2	329	1 IL2B_HORSE	Q9xsq5 equus cabal
30	150	6.6	918	1 IL6B_HUMAN	P40189 homo sapien
31	149.5	6.6	853	1 NCAL_BOVIN	P31836 bos taurus
32	148.5	6.5	329	1 IL2B_CANFA	Q28268 canis famil
33	148	6.5	335	1 IL2B_MOUSE	P43432 mus musculus

RESULT 1

ID	IL6A_MOUSE	STANDARD;	PRT;	460 AA.
AC	P22272;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Interleukin-6 receptor alpha chain precursor (IL-6R alpha) (IL-6R 1).			
GN	IL6RA OR IL6R.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BAIB/C; TISSUE=Spleen;			
RX	MEDLINE=90278354; PubMed=2112585;			
RA	Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T., Kishimoto T.;			
RT	"Functional murine interleukin 6 receptor with the intracisternal A particle gene product at its cytoplasmic domain. Its possible role in plasmacytomagenesis";			
RT	J. Exp. Med. 171:2001-2009(1990).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C3H; TISSUE=Liver;			
RA	Fiorillo M.T., Ciliberto G., Dente L.;			
RL	Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.			
CC	!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOIESIS.			
CC	!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY SIMILARITY).			
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.			
CC	!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X51975; CAA36237.1; -			
DR	EMBL; X53802; CAA37810.1; -			
DR	PIR; JLO144; JLO144.			
DR	PIR; JLO145; JLO145.			
DR	PIR; S14543; S14543.			
DR	HSSP; P16471; 1BP3.			

P46658 cercocebus
P13596 rattus norv
P13591 homo sapien
Q99062 homo sapien
Q9qzs7 mus musculus
Q9r044 rattus norv
P10586 homo sapien
Q00560 mus musculus
P43703 mus musculus
P48356 mus musculus
P42702 homo sapien
P16882 mus musculus

ALIGNMENTS

DR MGD; MGI:105304; IL6ra.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Signal.
FT CHAIN 1 19 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 20 460 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 20 364 POTENTIAL.
FT DOMAIN 365 385 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 386 460 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 40 99 BY SIMILARITY.
FT DISULFID 25 190 BY SIMILARITY.
FT DISULFID 47 92 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 17.48; Score 395.5; DB 1; Length 460;
Best Local Similarity 30.78; Pred. No. 2.4e-20;
Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;

Qy 1 MSSCSGLSRVLVAVALVASSPCPOAGPPGVQYQGPSVKLCPCGVTAGDPVS-- 58
Db 2 LTVGCTLLVALLAAPAVALLGS--CRALEVANGTVISLPATVTLICPGKEAGNVTH 59
Qy 59 WFRGEKLLGCPD-SGLGHLVLQAQDSTDEGYICQTLGALGGVTLQLGYPPARPV 117
Db 60 WYSGS-----QNRWTTTGNLTVLRLDVLQSLDGTGLC-SLNDHLVGVTVPLLDVDPPEPK 114
Qy 118 VSC-QAADYENFSTWSPSOISGLPTRYLTYSRKTKVLGADSORSPSTGWPQCP-QDPL 175
Db 115 LSCFKNPLVNAICEWRSPSTPS-PTTKAVLVFAKKI-----NTNGKSDFOVPCQYSQQL 168
Qy 176 GAARCVVHGAFFWFOYRI-NVTEYNPLGASTRLLDV--SLQSLRPPDPPOGLRVESVPGY 232
Db 169 KSFSCQVEILBGDKVYHIVSLVCVANSVSKSHNEAFSLK-WQPDPPANLVSAIPGR 227
Qy 233 PRLRLASWTYPASWPCQPHLLKFLRQYRPAQHAPWS-----TVEPAGLEEVITDAVAG 286
Db 228 PRLKLVSMQHPETWD-PSYLLQLQRLRYR-----PVWSKEFTVLLLPVAQYQCVIHDALRG 282
Qy 287 LPHAVRVYSARDFLDAGTWSTWSPAWGTTPSTGTIPKEIPA---WGQLHTQPEVEPQVDS 343
Db 283 VKHVQVVGKEELDGLGWSESPVETGPIAE-PRTPAGILMNP--TQVSVE---DS- 335
Qy 344 APPRSLQPHRLDHRD-----SVEQVAVLA-----SLGILSPGLVAGALALGLW--- 390
Db 336 -----ANHEDQVESSTEATSVLAPVQESSMSLPTFL-VAGSLAFLGLLVCV 381
Qy 391 ---LRLRGKGD-----GSPKPGFLASVIVPDRRPGAPN 421
Db 382 FTILRLQKWKSEAEKESKTTSPPPPPYSGLPKLPTPLVPLLTTPHSSGSDN 433

RESULT 2
CNTR_RAT
ID CNTR_RAT STANDARD; PRT; 372 AA.
AC Q08406;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE GN CNTRF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93152175; PubMed=8381290;
RA Ip N.Y., McClain J., Barrezuela N.X., Aldrich T.H., Pan L., Li Y.,
RA Wiegand S.J., Friedman B., Davis S., Yancopoulos G.D.;
RT "The alpha component of the CNTRF receptor is required for signaling
RT and defines potential CNTRF targets in the adult and during
RT development.";
RL Neuron 10:89-102(1993).
RN [2]
RP SEQUENCE OF 185-277 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93211934; PubMed=8460125;
RA Clatterbuck R.E., Price D.L., Koliatsos V.E.;
RT "Ciliary neurotrophic factor prevents retrograde neuronal death in
RT the adult central nervous system.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2222-2226(1993).
CC -!- FUNCTION: BINDS TO CNTRF (GPA). THE ALPHA CHAIN PROVIDES THE
CC RECEPTOR SPECIFICITY.
CC -!- SUBUNIT: HETEROPRIMER OF THE ALPHA CHAIN, LIFR AND GPI30.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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or send an email to license@isb-sib.ch).

EMBL; S54212; AAB25290.1; -
EMBL; S57711; AAB25918.1; -
PIR; A47387; A47387.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 342 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
FT PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 201 302 FIBRONECTIN TYPE-III.
FT DISULFID 46 89 POTENTIAL.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 342 342 GPI-ANCHOR (POTENTIAL).
FT CONFLICT 261 261 N -> D (IN REF. 2).
SQ SEQUENCE 372 AA; 40822 MW; 3B87EE63923FB149 CRC64;

Query Match 17.28; Score 392; DB 1; Length 372;
Best Local Similarity 31.9%; Pred. No. 3.2e-20;

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Matches 113; Conservative 49; Mismatches 164; Indels 28; Gaps 12;
Qy 1 MSSSCGSLRVLAVATATVAVATASPCQAWGPGVQYQGRSVKLCPCPGVTAGDPVSWF 60
Db 1 MAASVPWACCAVLAATAAATVQKHSPQ--APHVQYERLGTDTVPCGTASWDAATW 58
Qy 61 RDGEFKLQGGSLGHELVLAQADSTDEGTIYICQTLDG-ALGGTIVTLQGLYPPARPVYS 119
Db 59 VNGTD---LAPDLNGSLILRSLGSLGLYACFHRDWHLRHQVLLHVLGPPREPVL 115
Qy 120 COADY-ENFSCWSPSISGLPRYLTSYRKVILGADSORRSPSTGFWPCQDPLGA 178
Db 116 CRSNTPKGYFCSWHL---APT-YIPNTFNVTLHGSKM-----MVCEKDPALK 162
Qy 179 RCVVHGAEFWS--OYRINVTNPGLGASTRLDVSLSQILRPDPPOGLRVESVGP 236
Db 163 RCHRYMHLFTIKYKVISVSNALGHTNTAITDEFTIVRDPDPNVVAVPVSNP 222
Qy 237 RASWTYPASWPCQPHFLKFLQYRPAQHAPWSTVEPA-GLVEEITDAVAGLH 295
Db 223 EVTWQTPSTWDPESFPLKFLRYRPLLDQWQHVLSNGTAHTITDAYACKEXII 282
Qy 296 RDLFDAGTWSWSEAWGTPSTGIPKEIPAWGQLHTQPEVDPQVDSAPP 349
Db 283 KD-NEIGTWSWVAHAATPWTEE-PRHLTTEAQ---APETTTSTTSSLA 331
RESULT 3
IL6A_RAT STANDARD; PRT; 462 AA.
AC P22273;
AT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN IL6R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344; TISSUE=Liver;
RX MEDLINE=91060602; PubMed=2174054;
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RL rat liver interleukin 6 receptor.";
RL J. Biol. Chem. 265:19853-19862(1990).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA Gibson T.;
RL Unpublished observations (FEB-1995).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
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CC -----
DR EMBL: M58587; AAA41431.1; -.
DR PIR: A37986; A37986.
DR HSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Signal.
FT CHAIN 1 19
FT DOMAIN 20 462
FT TRANSMEM 20 364
FT DOMAIN 365 385
FT DOMAIN 386 462
FT DOMAIN 40 99
FT DISULFID 25 190
FT DISULFID 47 92
FT DISULFID 117 128
FT DISULFID 162 173
FT CARBOHYD 32 32
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 150 150
FT CONFLICT 227 261
FT FT
FT SQ SEQUENCE 462 AA; 50398 MW; A4D6064CEDC0537D CRC64;
Query Match 17.2%; Score 390.5; DB 1; Length 462;
Best Local Similarity 30.8%; Pred. No. 5.2e-20;
Matches 144; Conservative 55; Mismatches 183; Indels 85; Gaps 25;
Qy 1 MSSSCGSLRVLAVATATVAVATASPCQAWGPGVQYQGRSVKLCPCPGVTAGD--PVS 58
Db 2 LAVGCTLLVALLAAPAVALVLS--CRALEVANGVTVSLPGATVTLICPKGAAGNATH 59
Qy 59 WFDGEPKLLQGPD--SGLGHELVLAQADSTDEGTIYICQTLDGALGTTVTLQGLYPPARPV 117
Db 60 WYSGS-----OSREWTTTGTNTLVLRVAVQVNDTGHVLC-FLDDHLVGTVPLLVDPPEEPK 114
Qy 118 VSC-QAADYENFSCWSPSISGLPRYLTSYRKKTIVLGADSORRSPSTGFWPCP-QDPL 175
Db 115 LSCFKNPLVNAFCEWHPSSTPS-PTTKAVMFAKKI-----NTTNGKSDFOVPCQYSOOL 168
Qy 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLGASTRLDVSLSQSI--LRDPDPQGLRVESVPGY 232
Db 169 KSFSEVEILEGDKYVHIVSLCVANSVG--SRSSHNVFQSLKMWQPPDPANLVWSAIPGX 227
Qy 233 PRRLRASWTYPASWPCQPHFLKFLQYRPAQHAPWAS--TVEPAGLEE--VITDAVAG 286
Db 228 PRWLKVSQWQDPESWD-PSYILLQFELRYR---PWSKXFTVWPVLPVQVHQHCVIHDALRG 282
Qy 287 LPHAVRVSARDFDAGTWSWSEAWGTPSTGIPKEIPAWGQLHTQPEVEPQVDSAPP 346
Db 283 VKHVQVQVKGKEEFDIGQWKSSEVETGTP-----W---LAEPTTTPAGTGNPT 328
Qy 347 RPSLQPHRLDHRD-----SVEQVAVLA-----SLGILSFLGLVAGALALGLW----- 390
Db 329 QVSVEDYD---NHEDQYGSSTEATSVLAPVQSGSSPIPLPTFL-VAGGSLAFGLLLCVFTI 384
Qy 391 LRLRRGGKD-----GSPKPGFLASVIVPDRPAGPN 421
Db 385 LRLKKKKWSQAEKSKETTSPPPPYPLGPKLPTFL--LVPLLTSPSGSHN 429
RESULT 4
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ID	CNTR_HUMAN	STANDARD;	PRT;	372 AA.
AC	P26992;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ciliary neurotrophic factor precursor (CNTRF alpha).			
GN	CNTRF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=91289158; PubMed=1648265;			
RA	Davis S., Aldrich T.H., Valenzuela D.M., Wong V., Furth M.E.,			
RA	Squinto S.P., Yancopoulos G.D.;			
RT	"The receptor for ciliary neurotrophic factor.";			
RL	Science 253:59-63(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=95293367; PubMed=7774913;			
RA	Valenzuela D.M., Rojas E., le Beau M.M., Espinosa R.,			
RA	Brannan C.A., McClain J., Masiakowski P., Ip N.Y., Copeland N.G.,			
RA	Jenkins N.I., Yancopoulos G.D.;			
RT	"Genomic organization and chromosomal localization of the human and			
RT	mouse genes encoding the alpha receptor component for ciliary			
RT	neurotrophic factor.";			
RL	Genomics 25:157-163(1995).			
CC	!- FUNCTION: BINDS TO CNTRF (GPA). THE ALPHA CHAIN PROVIDES THE			
CC	RECEPTOR SPECIFICITY.			
CC	!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.			
CC	!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.			
CC	!- TISSUE SPECIFICITY: NERVOUS SYSTEM AND SKELETAL MUSCLE.			
CC	!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC	!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL	M73238; AAA35707.1;			
DR	EMBL; L38025; AAA91337.1;			
DR	EMBL; L38022; AAA91337.1; JOINED.			
DR	EMBL; L38023; AAA91337.1; JOINED.			
DR	EMBL; L38024; AAA91337.1; JOINED.			
DR	PIR; A40854; UHHUCN.			
DR	Genew; HGNC:2170; CNTRF.			
DR	MIM; 118946;			
DR	InterPro; IPR002996; CRIA.			
DR	InterPro; IPR003961; FN_III.			
DR	InterPro; IPR003530; Hemtopopn_L_F3.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003598; Ig_c2.			
DR	Pfam; PF000041; fn3.1.			
DR	Pfam; PF000047; ig; 1.			
DR	SMART; SM00060; FN3; 1.			
DR	SMART; SM00408; IGC2; 1.			
DR	PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.			
DR	Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 342			
FT	PROPEP 343 372			
FT	DOMAIN 39 96			
FT	DOMAIN 201 302			
FT	DISULFID 46 89			
FT	CARBOHYD 60 60			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			


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IL6A_PIG
ID IL6A_PIG STANDARD: PRT; 467 AA.
AC O18796;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN IL6R.
OS Sus scrofa (Fig.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN SEQUENCE FROM N.A.
RA Morris K.R., Strom A.D.G.;
RT "Cloning and expression of biologically active porcine IL-6 receptor
alpha chain.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RP [2]
RN SEQUENCE OF 123-186 FROM N.A.
RC TISSUE=Liver;
RA Klir J.J., Matteri R.L.;
RT "Partial cDNA sequence of porcine interleukin 6 receptor.";
RN Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC REACTIONS AND HEMATOPOIESIS.
CC -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL; AF147881; AAF73109.1; -.
DR EMBL; AF015116; AAB70916.1; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 366 386 POTENTIAL.
FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 25 193 BY SIMILARITY.
FT DISULFID 47 96 BY SIMILARITY.
FT DISULFID 121 132 BY SIMILARITY.
FT DISULFID 165 176 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 467 AA; 51066 MW; A2B0B884EF21C502 CRC64;

Query Match 14.4%; Score 326.5; DB 1; Length 467;
Best Local Similarity 28.2%; Pred. No. 1.4e-15;
Matches 129; Conservative 56; Mismatches 203; Indels 69; Gaps 20;

QY 12 LVAVATALVSASSPCP-QAWGPPG-----VOYGOPGRSVKLCCEGVTAGD--PVSW 59
DB 1 MLAVGCAQTALLAAGPMALAPRGCSKLEVAQDVLTSLPGASVTLTCPEGEPGDNATHW 60
QY 60 FR----DGEPKLLQGDGSLGHELVLAQADSTDEGTICOTLDGALGGTIVTLQLGYPPAR 115
DB 61 VLNRQVTGSP---DGRPAGVGRRLLLKSVQLSDSGNYSYQ-DGVPAGSVRLLVDPPEE 116
QY 116 PVVSC-QAADYENFSCWTSPQISGLPTRYLTSYRKKTIVLGDADSORRSP-STGPPPCPD 173
DB 117 POLSCFRKSPLSNVGCEWRP-----RSPSPPTTKAVLLVRKFQNSFVEQFPC-QY 167
QY 174 PLGAAR--CVVHGAEFWQYRI-NVTEYNPLGA-STRLLDVSLSQSLRLRDPDQGLRVESV 229
DB 168 SLEAQRFFCQIAVPEGDNSFHIVLCVANSAGSQSTPTQTFEGYGLQDPPVNIIVSAV 227
QY 230 PGYPRRLRASWTYPASWPCQPHFLKFRILQYRPAQHAWSTVEPAGLEE--VITDAVAGL 287
DB 228 DRNPRWLSVTWQDPPSWNSY-FYRLQFELRYRAERSKFTTMMVKELQHHCIIHDAWSGM 286
QY 288 PHAVRSARDFLDAGTWTSPWANGTPTST-----GTIPKEIPAWQLHTQPEVEFQVDS 343
DB 287 RHVVLQRAQEEFGHGLSEWSQEVGTGIPWTESRSPAETELPLSTQAPTNNDEDEDISK 346
QY 344 APPRESLOPHRLDHRDVEQVAVLASIGLSLGLVAGALALGLWLRLRGG-----K 398
DB 347 ESANATSLP-----VODSASVPLPTFLVAGGSLAFGLTLCIGIILFRKKTGQLQALK 398
QY 399 DGS-----PKPGFLASVIVPDRRPGAPN 421
DB 399 EGKTNMHPYSILGQLVPERPKSTPVLVPLISPPVSPN 435

RESULT 8
PRLR_MELGA STANDARD: PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1987 (Rel. 35, Created)
DT 01-NOV-1987 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
prolactin receptor during various reproductive states in Meleagris
gallopavo.";
FT gallopavo.";
RL Biol. Repr. 55:1081-1090 (1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

```



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Db 134 SLET-----KTSASTYLLAKWSPPPLADVTNSHVYVYELRLKPEEKEWETVS-VGV 186
Qy 277 EE--VITDAVAGLPHAVRVARSARDFLDAGTWTWSPEAWGTSTGTIPKEIP 325
Db 187 QTQYKVNRLQAGVKYVQV--RCVLDIGSEWSEWSSERHIHPNGESPPEKP 235

RESULT 10
PRLR_CHICK
ID PRLR_CHICK STANDARD; PRT; 831 AA.
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Kidney;
RA MEDLINE=93075121; PubMed=1445292;
RX Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D13154; BAA02439.1; -.
DR PIR: JQ1655; JQ1655.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRI1.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315

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FT CARBOHYD 335 335 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7579IDCDBE9 CRC64;

Query Match 9.4%; Score 214; DB 1; Length 831;
Best Local Similarity 27.5%; Pred. No. 1.6e-07;
Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

Qy 113 PARP--VWSCQAADYENFCTWSPSOISGLPTRYLTSYRKKTVLGADSORRSPSTGPMWPCP 171
Db 28 PGKPKIIIRCSLEKETFSQWKPQSDGGLPTNYTLFYSK-----DSEEEI-----YECF 76
Qy 172 Q-DPLGAARCVV--HGAEFWQYRINVTENPLGAST---RLLDVSLQSLILRPDPPOGLR 225
Db 77 DYRTSGPNSCYFNKNHTSPWTTTNTATNEIGSNSSDPQYVDVT--SIVQGGSPVNL 134
Qy 226 VESVPGYPR-----LRASWTYPASWPCQPHFLKFLRQYPAQHPAWSVTEPAGLEE- 278
Db 135 LET-----KRSANIMYLWAKWSPLLADASSNHLHYELRIKPEKEWETIS-VGVQTP 188
Qy 279 -VITDAVAGLPHAVRVARSARDFLDAGTWTWSPEAWGTSTGTIPKEIPAWGOLHTQPEVE 337
Db 189 CKINRLNAGMRVQV--RCTLDPGSEWSEWSSERHILLPSQSGSPPEKPTIIKCRS-PEKE 245
Qy 338 -----POVDSPPAPRPSLQPHRLDLDRDSVEQV 366
Db 246 TFTCWKPKGLDGGHPTNVT-----LLYSKEGEQV 275

RESULT 11
PRLR_SHEEP
ID PRLR_SHEEP STANDARD; PRT; 581 AA.
AC Q46561; P79205; Q46574; Q46573; P79203; Q46569;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (OPR).
GN PRLR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Liver, and Mammary gland;
RX MEDLINE=98001468; PubMed=9343303;
RA Bignon C., Binard N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
and genomic analysis reveal that the two forms arise by different
alternative splicing mechanisms in ruminants and in rodents.";
RL J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
SEQUENCE OF 61-395 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
SPECIFICITY.
RC STRAIN=Scottish blackface; TISSUE=Anterior pituitary;
RX MEDLINE=99049302; PubMed=9832462;
RA Tortorese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;
RT "Detection of prolactin receptor gene expression in the sheep
pituitary gland and visualization of the specific translation of the
signal in gonadotrophs.";
RL Endocrinology 139:5215-5223(1998).
RN [3]
SEQUENCE OF 147-302 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
SPECIFICITY.
RC TISSUE=Corpus luteum, and Fetal liver;
RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
RT "Two forms of the prolactin receptor messenger ribonucleic acid are
present in ovine fetal liver and adult ovary.";
RL Endocrine 3:291-295(1995).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1/long/L-OPR (shown here),

```


Db 65 SSEVL-----GSGKTLTILVKEFEDAGHYTCRR-----GGEVLSQLLLHKNEDGIWST 114
QY 110 -----GYPPARPVWSCQAADYE-NFSCWTSPSQISGLPTRYLTSYKKTIVLGADSORRSP 163
Db 115 DILKKKEPENKNLVTCSEAKNYSGRFTCMW-----LTAISTDVNFYSKSHRGSS 162
QY 164 STGPWFPCQDPLGAARCVVHGAEFWSQYRINVTENPLGASTRLLDVS----- 211
Db 163 DPQGVTCGEATLSAERVKIEQREY-KKYSVQCOEDNACPTAEETLPITVVVDVAVHKLKYE 221
QY 212 -----LQSI LRPPQGLRVESVPGYPRRLRASWTYPASWPCOPH--FLKFRLOQYRP 262
Db 222 NYISSFFIRDI IKPDPKLNKMKP-SKTPQQVEVTWEYKPDW-STPHSYFSLTFSVQVQG 279
QY 263 AOHPAWSTVEPAGLEVIITDAVAGLPHAVRVARSARDFLDAGTWSTWS 308
Db 280 KKKKRSNTLH---VDKTSVTVCQKGVSVQVQARDRYNNSWSEWA 322

Search completed: January 17, 2003, 19:38:22
Job time : 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:37:20 ; Search time 22 Seconds
(without alignments)
1844.033 Million cell updates/sec

Title: US-09-924-338-2
Perfect score: 2275
Sequence: 1 MSSSCSGLSRVLVAVATALV.....KPGFLASVIPVDRRPGAPNL 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	2 I37891	interleukin-11 rec
2	1897	83.4	432	2 I48343	interleukin-11 rec
3	395.5	17.4	460	2 J10145	interleukin-6 rece
4	392	17.2	372	2 J38141	ciliary neurotroph
5	389.5	17.1	440	2 J10144	interleukin-6 rece
6	380	16.7	362	2 S60614	growth promoting a
7	379	16.7	372	1 UHHUCN	ciliary neurotroph
8	360	15.8	468	1 A41242	interleukin-6 rece
9	298.5	13.1	462	1 A37986	interleukin-6 rece
10	221	9.7	830	2 I50455	prolactin receptor
11	214	9.4	831	2 J01655	prolactin receptor
12	204.5	9.0	581	2 I45971	prolactin receptor
13	204	9.0	616	2 A30304	prolactin receptor
14	189	8.3	288	2 B59405	prolactin receptor
15	189	8.3	376	2 A59405	prolactin receptor
16	189	8.3	622	2 A40144	prolactin receptor
17	186	8.2	1265	1 A37967	prolactin receptor
18	183	8.0	310	2 A29884	neural cell adhesi
19	183	8.0	412	2 A41070	prolactin receptor
20	183	8.0	610	2 A34631	lactogen receptor
21	183	8.0	610	2 A36116	prolactin receptor
22	174	7.6	292	2 I77525	prolactin receptor
23	174	7.6	303	2 I77524	prolactin receptor
24	174	7.6	608	2 I53269	prolactin receptor
25	173.5	7.6	630	2 I51086	prolactin receptor
26	167.5	7.4	328	2 A38957	interleukin 12b pr
27	166.5	7.3	761	1 IJHUNG	neural cell adhesi
28	150	6.6	918	2 A36337	membrane glycoprot
29	149.5	6.6	853	1 IJUBNC	neural cell adhesi

ALIGNMENTS

RESULT 1

I37891
interleukin-11 receptor alpha chain - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
C:Accession: I37891; G01970; G01971
R:Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
Blood 86, 2534-2540, 1995
A>Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic
A:Reference number: I37891; MUID:95399754; PMID:7670098
A:Accession: I37891
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-422 <RES>
A:CROSS-references: EMBL:Z38102; NID:g995653; PIDN:CAA86224.1; PID:g995654
R:Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A:Reference number: G08959
A:Accession: G01970
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-422 <VAN>
A:CROSS-references: EMBL:U32323; NID:g975334; PIDN:AAB36491.1; PID:g975335
R:Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A:Reference number: G08961
A:Accession: G01971
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-422 <VA2>
A:CROSS-references: EMBL:U32324; NID:g975336; PIDN:AAB36492.1; PID:g975337
C:Genetics:
A:Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immu
F:120-310/Domain: cytokine receptor homology <CR>

Query Match 100.0%; Score 2275; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.6e-143;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSSSCSGLSRVLVAVATALV	ASSPCPOAWGPGVQYQOPGRSVKLCPCGVTAGDPVSNF	60
Db	1	MSSSCSGLSRVLVAVATALV	ASSPCPOAWGPGVQYQOPGRSVKLCPCGVTAGDPVSNF	60
Qy	61	RDEGPKLLQGPSGLGHELVLAQAADSTDEGT	YICQTLDGALGGTTLQGLGYPPARPVVSC	120
Db	61	RDEGPKLLQGPSGLGHELVLAQAADSTDEGT	YICQTLDGALGGTTLQGLGYPPARPVVSC	120
Qy	121	QAADYENFSCWSPSQISGLPTRYLTSYRKKT	VLGADSORRSPSTGWPCCPDPLGAARC	180
Db	121	QAADYENFSCWSPSQISGLPTRYLTSYRKKT	VLGADSORRSPSTGWPCCPDPLGAARC	180

interleukin 12 p40
neural cell adhesi
granulocyte colony
granulocyte colony
granulocyte colony
probable neural ce
leukocyte antigen-
lactogen receptor
glycoprotein I30 -
leukocyte antigen-
differentiation-st
leptin receptor, s
leptin receptor, s
leptin receptor, s
leptin receptor, s
leptin receptor, s

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QY 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCQPHEFLKFRLOYRPAQHPANSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
Db 241 TYPASWPCQPHEFLKFRLOYRPAQHPANSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
QY 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPPRLSLQHPRLLDHR 360
Db 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPPRLSLQHPRLLDHR 360
QY 361 DSVEQAVLASLGILSLFGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPGAP 420
Db 361 DSVEQAVLASLGILSLFGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPGAP 420
QY 421 NL 422
Db 421 NL 422

RESULT 2
I48343
Interleukin-11 receptor alpha-chain precursor - mouse
N:Alternate names: cytokine type 1 receptor
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C:Accession: I48343; S51619
R:Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossle
Dev. Biol. 166, 521-542, 1994
A:Title: etl2, a novel putative type-1 cytokine receptor expressed during mouse embryoge
A:Reference number: I48343
A:Accession: I48343
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Cross-references: EMBL:X74953; NID:G673437; PIDN:CAA52908.1; PID:G673438
R:Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.;
EMBO J. 13, 4765-4775, 1994
A:Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high
A:Reference number: S51619; MUID:95045367; PMID:7957045
A:Accession: S51619
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432 <HIL>
A:Cross-references: EMBL:U14412; NID:G576454; PIDN:AAA53248.1; PID:G576455
C:Genetics:
A:Gene: Et12/IL11
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
F:120-310/Domain: cytokine receptor homology <CRS>

Query Match 83.4%; Score 1897; DB 2; Length 432;
Best Local Similarity 83.5%; Pred. No. 1.8e-118;
Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSSCGSLRVLAVATALVSASSPCPAWGPVQYQGPGRSVKLCPCPGVTAGDPVSWF 60
Db 1 MSSSCGSLRVLAVATALVSASSPCPAWGPVQYQGPGRSVKLCPCPGVTAGDPVSWF 60
QY 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGYICOTLDGALGGTTLQLGYPARPVVC 120
Db 61 RDGSRLLQGPDSGLGHELVLAQVDSDEGYVCOTLDGVSQGMVTLKLGPPARPVVC 120
QY 121 QAADYENFSCWSPQISGLPTRYLTYSRKKTVLGADSORRSPSTGPWPCPDPLGAARC 180
Db 121 QAADYENFSCWSPQISGLPTRYLTYSRKKTVLGADSORRSPSTGPWPCPDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCQPHEFLKFRLOYRPAQHPANSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
```

```
Db 241 TYPASWPCQPHEFLKFRLOYRPAQHPANSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
QY 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPPRLSLQHPRLLD 358
Db 301 AGTWSANSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPPRLSLQHPRLLD 360
QY 359 HRDSVEQAVLASLGILSLFGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPG 418
Db 361 HRDPLEQAVLASLGILSLFGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPG 420
QY 419 APNL 422
Db 421 IPNL 424

RESULT 3
JL0145
Interleukin-6 receptor precursor (clone lambda 301) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0145; S14543
R: Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A:Reference number: JL0144; MUID:90278354; PMID:2112585
A:Accession: JL0145
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-460 <SUG>
A:Cross-references: GB:X51975; NID:949725; PIDN:CAA36237.1; PID:G49726
A:Experimental source: clone lambda 301
R: Florillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A:Description: Cloning and expression of murine IL-6 receptor.
A:Reference number: S14543
A:Accession: S14543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373, 'R', 375-460 <FIO>
A:Cross-references: EMBL:X53802; NID:G52692; PIDN:CAA37810.1; PID:G52693
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 17.4%; Score 395.5; DB 2; Length 460;
Best Local Similarity 30.7%; Pred. No. 5.8e-19;
Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;

QY 1 MSSSCGSLRVLAVATALVSASSPCPAWGPVQYQGPGRSVKLCPCPGVTAGDPVSWF 58
Db 2 LTVGCTLLVALLAPAVALVLGS--CRALEVANGTIVTSLPGATVTLICPGKEAAGNVTH 59
QY 59 WFRDGEPEKLLQGPDSGLGHELVLAQADSTDEGYICOTLDGALGGTTLQLGYPARPV 117
Db 60 WYVSGS-----QNRWTTTGNLVLRLVDQLSDTDGYLC--SLNDHLVGVPLLVDPVPEEPK 114
QY 118 VSC-QAADYENFSCWSPQISGLPTRYLTYSRKKTVLGADSORRSPSTGPWPCPDPL 175
Db 115 LSCFRKNPLVNAICEWRPSSTPS-PTTKAVLFAKKI-----NTTNGKSDFOVPCQYSQOL 168
QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPILGASTRLLDV--SLQSLRDPDPOGLRVESVPGY 232
Db 169 KSFSCQVEILEGDKVYHIVSLCVANSVSGSKSHNEAFHSLK-MVQPDPPANLVVSAIPGR 227
QY 233 PRRLRASWTYPASWPCQPHEFLKFRLOYRPAQHPANSTVEPAGLEEVITDVAAG 286
Db 228 PRWLKVSQHPETWD-PSYLLQFQLRYR---PWSKEFTVLLLPVQAQYOCVTHDALRG 282
```

C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin-like domain
C;Keywords: growth factor receptor

C;Comment: This growth factor receptor does not have a tyrosine kinase domain.

C;Genetics:
A;Gene: GDB:IL6R
A;Cross-references: GDB:127966; OMIM:147880
A;Map Position: 1q21-1q21
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-468/Product: interleukin-6 receptor #status predicted <MAT>
F;386-462/Domain: intracellular #status predicted <INT>
F;47-92/Disulfide bonds: #status predicted <IMM2>
F;121-309/Domain: cytokine receptor homology <CRS>
F;364-386/Domain: transmembrane #status predicted <TM>
F;387-468/Domain: intracellular #status predicted <INT>
F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.8%; Score 360; DB 1; Length 468;
Best Local Similarity 28.4%; Pred. No. 1.3e-16;
Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

Qy 1 MSSSCSLRVLAVATATYALVSSPCQAWGPPGVQYQCPGRSVKLCPCPGVTAGD--PVS 58
Db 2 LAVGCTLLVALLAAPAVALVGS--CRALEVANGTSTSLPGCATVTLICPGKEAAGNATHI 59

Qy 59 WFRDGEPEKLLQGPD-----SGLGHELVLAQADSTDEGTYICOTLDGALGGTIVTLQGL 110
Db 60 W-----VLRKPAAGSHPSWAGMGRLLRSVQLHDSGNYSCYRA-GRPAGTVHLLVD 111

Qy 111 YPPARPVVSC-0AADYENFSCVSPQISGLPTRYLTYSRKKTVLGADSORRSPSTG-PW 168
Db 112 VPPEEPQLSCFRKPSLVNVCEWGPSTPSLT-----KAVLLVRKFNQSPAEDEFQ 163

Qy 169 PC-----QDDPLGAARCVVHGAEFFNSQRYINVTENPLGAS--TRLLDVSLOSILRDP 223
Db 164 PCQYSQSKFSCOLAVPEGDS--SFYIVSMCVASSVSGSKFSTQTTFQGGILOPDP 221

Qy 224 LRVESVPGYPRRLRASWTYPASWPCQPHFLKFRLOVRPAQHPAWSTVEPAGLEE--VIT 281
Db 222 ITVTAVARNPRLSVTQDPHSMN--SFYRLRFELRYRAERSKFTTVMVKDLQHHCVIH 280

Qy 282 DAVAGLPHAVRSARDLDAGTWTSPAEAGTSTGTIPKEIPAMQQLHTQPEVEQVD 341
Db 281 DAWSLRHVVQLRAEEFQGESEWSEWSPAEAGTPTWES-----RSPPAENEVS 328

Qy 342 SPAPRPSLOPHRLLDHRSQEVAV---LASIGILSFLGLVAGALAG----- 388
Db 329 TPMQALTNKDDNLL-PRSANATSLPVQDSSSVPLPTFL-VAGGSLAFGLTLCIAIVL 386

Qy 389 ----LW-LRLRRGGKDGSPKFGFLASVIPVDRP 417
Db 387 RFKKTWKLRLAKCKTSMHPYSLGLVPERPRP 420

RESULT 9
A37986
interleukin-6 receptor precursor - rat
N;Alternate names: IL-6 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A37986
R;Baumann, M.; Baumann, H.; Fey, G.H.
J. Biol. Chem. 265, 19853-19862, 1990
A;Title: Molecular cloning, characterization and functional expression of the rat liver
A;Reference number: A37986; MUID:91060602; PMID:2174054
A;Accession: A37986
A;Molecule type: mRNA
A;Residues: 1-462 <BAU>
A;Cross-references: GB:M58587; GB:J05668; NID:g204921; PID:AAAA1431.1; PID:g204922
C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is es
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin protein
F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-462/Product: interleukin-6 receptor #status predicted <MAT>
F;20-362/Domain: extracellular #status predicted <EXT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;363-385/Domain: transmembrane #status predicted <TM>
F;386-462/Domain: intracellular #status predicted <INT>
F;47-92/Disulfide bonds: #status predicted

Query Match 13.1%; Score 298.5; DB 1; Length 462;
Best Local Similarity 27.2%; Pred. No. 1.6e-12;
Matches 132; Conservative 50; Mismatches 181; Indels 123; Gaps 25;

Qy 1 MSSSCSLRVLAVATATYALVSSPCQAWGPPGVQYQCPGRSVKLCPCPGVTAGD--PVS 58
Db 2 LAVGCTLLVALLAAPAVALVGS--CRALEVANGTSTSLPGCATVTLICPGKEAAGNATHI 59

Qy 59 WFRDGEPEKLLQGPD-----SGLGHELVLAQADSTDEGTYICOTLDGALGGTIVTLQGL 117
Db 60 WYVSGS-----QSRWMTTGTNTLVLRVAVQVNDTGHYLC-FLDDHLVGTIVPLLVDPPEEPK 114

Qy 118 VSC-0AADYENFSCVSPQISGLPTRYLTYSRKKTVLGADSORRSPSTGPMPCP-QDPL 175
Db 115 LSCFRKNPLVNAFCWEHPSPSTPS-PTTKAVMFARKI-----NTNGKSDFOVPCQYSQQL 168

Qy 176 GAARCVVHGAEFFNSQRYI-NVTENPLGASTRLDVSLSQSI--LRPDPQGLRVESVPG- 231
Db 169 KSFCEVEILGDKVYHIVSLCVANSYG-SRSSHNVVFQSLKMQVOPPANLVVSAIPGS 227

Qy 232 -----YPRKRASWTYPASWPCQPHFLKFRLOVRPAQHPA 267
Db 228 LVGSKSVGKTLSPGTQVTTCCNSSTFDLYGQRTFTV-WPLQ-----VAQHQC 274

Qy 268 WSTVEPAGLEVIITDAVAGLPHAVRSARDLDAGTWTSPAEAGTSTGTIPKEIPAW 327
Db 275 -----VIHDALRGVHVQVKGKEEDIGQWSKSPSVETGTP-----W 312

Qy 328 QQLHTQPEVEQVDSPAPPESLOPHRLLDHRSQEVAVLA-----SVEQVAVLA-----SILGILSF 377
Db 313 --LAEPRTTTPAGTGNPTQVSVEDYD--NHEDQYSGSSTATSVLAPVQGSSTPIPLPTF 366

Qy 378 LGLVAGALAGLW-----LRLRRGGK-----GSPKPGFLASVIPVDR 415
Db 367 L-VAGGSLAFGLLGLCVFIILRLKRRKKWSQAEKSKTTPPPYPLGLPKPTFL--LVPLLT 423

Qy 416 RPAAPN 421
Db 424 PSGSHN 429

RESULT 10
I50455
prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C;Accession: I50455
R;Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin recepto
A;Reference number: I50455; MUID:94283267; PMID:7516866
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-830 <CHE>
A;Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C;Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>

Query Match 9.78%; Score 221; DB 2; Length 830;
Best Local Similarity 29.08; Pred. No. 4e-07;
Matches 67; Conservative 36; Mismatches 90; Indels 38; Gaps 12;

Qy 111 YPPARPVVSCQADYENFSCVSPQISGLPTRYLTYSRKKTVLGADSORRSPSTGPMPCP 170

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Db 27 YGPKIIRCRSLERETFCWMMKPGSDGLPTNYTLFYSK-----DSEKI-----YEC 75
QY 171 PDPL-GAARCVV--HGAEFWSQYRINTEVNPGLAST---RLLDVSLQSLRPDPPOGL 224
Db 76 PDYMGSGNSCYFEDKXNHPWTYITVYAMNEIGNSSDPOYVDVT--SIVQDPAPVNL 133
QY 225 RVESVPGYPRRLRASWY-PASWPCQP-----HFLKFLRQYRPAQHPAWSTVEPAGL 276
Db 134 SLET-----KTSASTTYLLAKWSPPLADVTSNSHVYELRLKPEKEWEIVS-VGV 186
QY 277 EE--VITDAVAGLPHAVRVSRDGLDAGTWSWPEANGTPTSTGIPKEIP 325
Db 187 QYQVKNRLQAGVYVQV--RCVLDIGSEWSSSRIHIHPNGESPPEKP 235

RESULT 11
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R: Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121; PMID:1445292
A:Molecule type: mRNA
A:Residues: 1-831 <FAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: Kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal transducer #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (asn) (covalent)

Query Match 9.4%; Score 214; DB 2; Length 831;
Best Local Similarity 27.5%; Pred. No. 1.2e-06;
Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

QY 113 PARP-VVSCQAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORSPSTGWPWC 171
Db 28 PGKPKIIRCRSLERETFCWMMKPGSDGLPTNYTLFYSK-----DSEKI-----YEC 76

QY 172 Q-DPLGAARCVV--HGAEFWSQYRINTEVNPGLAST---RLLDVSLQSLRPDPPOGLR 225
Db 77 DYRTSGPNSCYFNKNHTSPWTNIITVATNEIGNSSDPOYVDVT--SIVQPGSPVNL 134
QY 226 VESVPGYPRR-----LRASWTPASWPCOPHLLKFLRQYRPAQHPAWSTVEPAGLEE- 278
Db 135 LET-----KRSANIMYLAKWSPPLDASSNHLHYELRIKPEKEWETIS-VGVQTO 188
QY 279 -VITDAVAGLPHAVRVSRDGLDAGTWSWPEANGTPTSTGIPKEIPAWQLHTQPEVE 337
Db 189 CKINRLNAGRYVQV--RCTLDPGSEWSSSRHILIPSGSPPEKPTTIKCRS-PERE 245
QY 338 -----POVDSAPPRLPQLPHRLHRDSVEQV 366
Db 246 TETCWMMKPGLDGGHTNYT-----LLYSKEGEQV 275

RESULT 12
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R: Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
```

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A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prola
A:Reference number: I45971; MUID:93246019; PMID:1338725
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:I02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRUR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 9.0%; Score 204.5; DB 2; Length 581;
Best Local Similarity 26.5%; Pred. No. 3.4e-06;
Matches 61; Conservative 36; Mismatches 92; Indels 41; Gaps 11;

QY 112 PPARP-VVSCQAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORSPSTGWPWC 170
Db 27 PPEKPKLVKCRSPGKETFTCWEPGADGGLPTNYTLTYHKE-----GETLIHEC 75

QY 171 PQDPLGAARCVVHG---AEFWSQYRINTEVNPGL-ASTRLDVSLSQSLRPDPPOGLRV 226
Db 76 PDYKTGPNSCYFESKKTHTSIKMWVITVNAINQMGISSDPLYVHYVYIPEPEPANLTL 135

QY 227 ESVPGYPRR--LRASWTP-----ASWPCOPHLLKFLRQYRPAQHPAWS---TVEPAG 275
Db 136 ELKHPEDRKPKYLWIKWSPPTMTDVKSGW-----PIQVEIRLKEKATDWTHTLQQTQ 190

QY 276 LEEVITDAVAGLPHAVRVSRDGLDAGTWSWPEANGTPTSTGIPKEIP 325
Db 191 LK--IFNLYPGQKYLVOIRCKP--DHGYWSEWSPE-----SSIQIPNDPF 231

RESULT 13
A30304
prolactin receptor 2 precursor - rabbit
N:Alternate names: prolactin receptor, mammary gland
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C:Accession: A30304; A60380
R: Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Bout
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A:Title: Identification and sequence analysis of a second form of prolactin receptor
A:Reference number: A30304; MUID:89184578; PMID:2928321
A:Accession: A30304
A:Molecule type: mRNA
A:Residues: 1-616 <EDE>
A:Cross-references: GB:J04510; NID:g165669; PIDN:AAA31457.1; PID:g165670
R: Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Biochem. 22, 1089-1095, 1990
A:Title: Purification and partial sequence of the rabbit mammary gland prolactin rece
A:Reference number: A60380; MUID:91146782; PMID:2289615
A:Accession: A60380
A:Molecule type: protein
A:Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX',
A:Note: The amino end of the mature protein was blocked
C:Superfamily: cytokine receptor homology
C:Keywords: blocked amino end; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:235-258/Domain: transmembrane #status predicted <TM>
F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 9.0%; Score 204; DB 2; Length 616;
Best Local Similarity 27.7%; Pred. No. 3.9e-06;
Matches 66; Conservative 29; Mismatches 95; Indels 48; Gaps 13;

QY 112 PPARP-VVSCQAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORSPSTGWPWC 170
Db 27 PPGKPKFIFKCRSPGKETFTCWWRPGADGGLPTNYTLTYHKE-----GETITHEC 75

QY 171 PQDPLGAARCVVHG---AEFWSQYRINTEVNPGLAST---RLLDVSLQSLRPDPPOGL 224
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Db 76 PDYKGTGPNSCYFSKKHTSIWTIIIVTNATNQSSVSPRYVDVTV--IVEPDPVNL 133
QY 225 RVESVPCYPRR--LRASWTYP-----ASWPCQPHFLKRLQYRPAQHAWSTVEAGL 276
Db 134 TLEVKHEDRRPYLWVKWLPPTLVDRVSGW-----LTLQYEIRLKPKEAAEWET-HEAGQ 187
QY 277 EE--VITDVAAGLPHAVRVVSARDPLDAGTWSWSPAEWGPSTGTIP-----KEIPAW 327
Db 188 QTQPKILSLYPGQKYLQVRCRP--DHGFWSVMSPE-----SSIIQINDFTMKDITW 238

RESULT 14

B59405

prolactin receptor short form Slb precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002

C:Accession: B59405; B49400

R/Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin receptor

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: B59405

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU1>

A:Cross-references: GB:AF214012; PIDN:AF214012.1

R/Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: B49400

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU2>

A:Cross-references: GB:AF214012; PIDN:AF214012.1

A:Comment: This is one of the short forms (Slb and Slb) of the human prolactin receptor

ta-casien gene promoter activation, with Slb more effective than Slb. However, their lig

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Superfamily: cytokine receptor homology

C:Keywords: glycoprotein; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-288/Product: prolactin receptor, short form Slb #status predicted <MAT>

F;36-221/Domain: cytokine receptor homology <CRS>

F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 189; DB 2; Length 288;

Best Local Similarity 28.2%; Pred. No. 1.7e-05;

Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;

QY 112 PPARP-VVSCQADYENFSCSTWSPSQISGLPTRYLTYSYRKTKVLGADSQRRSPSTGPWPC 170

Db 27 PPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNYSLT-----HREGETLMHEC 75

QY 171 PQDPLGAARCVVHGAEP---WSQYRINVTENVPLGAS--TRLLDVSLOSILRPDPQGLRV 226

Db 76 PDYITGPNNSCHFGCKQYTSMMRTYIMMVNATNQSSFSDELYVDVTVIVQDPDPLEAV 135

QY 227 ESVPYGPYPRR--LRASWTYP-----ASWPCQPHFLKRLQYRPAQHAWSTVEPAG--L 276

Db 136 EVKQPEDRKPYLWKNSPPTLIDLKTGW-----FTLLYEIRLKPKEAAEWI-IHFAGQQT 189

QY 277 EEVITDVAAGLPHAVRVVSARDPLDAGTWSWSP 309

Db 190 EFKILSLHPGQKYLQVRCRP--DHGYWSAWSP 220

RESULT 15

A59405

prolactin receptor short form Slb precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
C:Accession: A59405; A49400
R/Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin rec
A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: A59405
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HU1>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
R/Hu, Z.Z.
submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: A49400

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU2>

A:Cross-references: GB:AF214012; PIDN:AF214012.1

A:Comment: This is one of the short forms (Slb and Slb) of the human prolactin recept
eta-casien gene promoter activation, with Slb less effective than Slb. However, their
ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #e

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Superfamily: cytokine receptor homology

C:Keywords: glycoprotein; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-376/Product: prolactin receptor, short form Slb #status predicted <MAT>

F;36-221/Domain: cytokine receptor homology <CRS>

F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 189; DB 2; Length 376;

Best Local Similarity 28.2%; Pred. No. 2.2e-05;

Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;

QY 112 PPARP-VVSCQADYENFSCSTWSPSQISGLPTRYLTYSYRKTKVLGADSQRRSPSTGPWPC 170

Db 27 PPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNYSLT-----HREGETLMHEC 75

QY 171 PQDPLGAARCVVHGAEP---WSQYRINVTENVPLGAS--TRLLDVSLOSILRPDPQGLRV 226

Db 76 PDYITGPNNSCHFGCKQYTSMMRTYIMMVNATNQSSFSDELYVDVTVIVQDPDPLEAV 135

QY 227 ESVPYGPYPRR--LRASWTYP-----ASWPCQPHFLKRLQYRPAQHAWSTVEPAG--L 276

Db 136 EVKQPEDRKPYLWKNSPPTLIDLKTGW-----FTLLYEIRLKPKEAAEWI-IHFAGQQT 189

QY 277 EEVITDVAAGLPHAVRVVSARDPLDAGTWSWSP 309

Db 190 EFKILSLHPGQKYLQVRCRP--DHGYWSAWSP 220

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Job time : 26 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:38:14 ; Search time 13 Seconds
(without alignments)
645.287 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSGSLRVAVATLV.....KPGFLASVIPDRRPGAPNL 422

Scoring table: BLOSUM62

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Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PublishedApplications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1831	80.5	441	10	US-09-924-338-4
3	339	14.9	1158	9	US-09-935-868-26
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5	329.5	14.5	360	9	US-09-935-868-15
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7	315	13.8	315	9	US-09-935-868-16
8	255.5	11.2	229	9	US-10-000-776-10
9	255.5	11.2	229	9	US-09-791-497-12
10	212.5	9.3	389	10	US-09-880-578-27
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16	211.5	9.3	422	9	US-09-944-896-32
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20 211.5 9.3 422 10 US-09-866-028-32 Sequence 32, Appl
21 211.5 9.3 422 10 US-09-944-449-32 Sequence 32, Appl
22 211.5 9.3 422 10 US-09-944-457-32 Sequence 32, Appl
23 211.5 9.3 422 10 US-09-944-862-32 Sequence 32, Appl
24 211.5 9.3 422 10 US-09-945-587-32 Sequence 32, Appl
25 211.5 9.3 422 10 US-09-945-015-32 Sequence 32, Appl
26 211.5 9.3 422 10 US-09-944-396-32 Sequence 32, Appl
27 211.5 9.3 422 10 US-09-944-097-32 Sequence 32, Appl
28 211.5 9.3 422 10 US-09-944-432-32 Sequence 32, Appl
29 211.5 9.3 422 10 US-09-943-762-32 Sequence 32, Appl
30 211.5 9.3 422 10 US-09-944-654-32 Sequence 32, Appl
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37 210.5 9.3 392 10 US-09-880-578-18 Sequence 18, Appl
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40 209.5 9.2 405 9 US-10-074-901-2 Sequence 2, Appl
41 209.5 9.2 413 10 US-09-037-657-13 Sequence 13, Appl
42 209.5 9.2 425 10 US-09-037-657-15 Sequence 15, Appl
43 207.5 9.1 303 10 US-09-880-578-23 Sequence 23, Appl
44 207.5 9.1 385 10 US-09-880-578-19 Sequence 19, Appl
45 207.5 9.1 385 10 US-09-880-578-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-924-338-2
; Sequence 2, Application US/09924338
; Patent No. US20020082233A1
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/924,338
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/151,102
; FILING DATE: 1998-09-10
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-924-338-2
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Best Local Similarity 100.0%; Pred. No. 5e-144;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 TYPASWPCQPHFLKFRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
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Db 301 AGTWSTWSPAWGTPSTGTIPKEIPAWCOLHTQPEVQVDSPPAPRPSLQPHRLLDHR 360
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Oy 421 NL 422
Db 421 NL 422
RESULT 2
US-09-924-338-4
; Sequence 4, Application US/09924338
; Patent No. US20020082233A1
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/924,338
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/151,102
; FILING DATE: 1998-09-10
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-924-338-4
Query Match      80.5%; Score 1831; DB 10; Length 441;
Best Local Similarity 83.1%; Pred. No. 1.5e-114;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;
Oy 16 ATALVSASSPCPAWPGVQYQPGRSVKLCCPGVTAGDPVSWFRDGEPLKLLQGGDGL 75
Db 25 ATALVSASSPCPAWPGVQYQPGRVMLCCPGVSAGTVPVFRDGDRLQGGDGL 84
Oy 76 GHELVLAQADSTDEGTYICQTLGALGGTTLQGYPPARPVWSCQAADYENFSCWSPS 135
Db 85 GHELVLAQVDSDEGTYVQTLGCVSGMWTLKLGFFPARPEVSCQAVDYENFSCWSPG 144
Oy 136 QISGLPTRYLTYSRKKTIVLGADSORRSPSTGPPCPQDPPLGAARCVVHGAEFWSQYRIN 195
Db 145 QVSGLPTRYLTYSRKKTLPGAESQRESPTGPPCPQDPPLGASRCVVHGAEFWSEYRIN 204
Oy 196 TEVNPGLASTRLLDVLSQSLTRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
Db 205 TEVNPGLASTRLLDVLRQSLTRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
Oy 256 FRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLDAGTWSTWSPAWGTP 315
Db 265 FRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLDAGTWSTWSPAWGTP 324
Oy 316 STGTIPKEIPAWCOLHTQ--PEVEPQVDSPPAPRPSLQPHRLLDHRDSVEQVAVLASLG 373
Db 325 STGTIPKEIPAWCOLHTQ--PEVEPQVDSPPAPRPSLQPHRLLDHRDSVEQVAVLASLG 384
Oy 374 ILSFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVTPVDRRPGAPNL 422
Db 385 ILSFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVTPVDRRPGAPNL 433
RESULT 3
US-09-935-868-26
; Sequence 26, Application US/09935868
; Patent No. US2002016490A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-26
Query Match      14.9%; Score 339; DB 9; Length 1158;
Best Local Similarity 30.4%; Pred. No. 4.1e-15;
Matches 112; Conservative 45; Mismatches 169; Indels 42; Gaps 14;
Oy 5 CSGLSRVLAVATLVASSPCPAWPGVQYQPGRSVKLCCPGVTAGD--PVSWFRD 62
Db 6 CALLAALLAAPGAAL--APRRCPAQAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW--- 60
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QY	63	GEPLKGGPD-----SGLGHELVLAAQADSTDEGTYICQTLDGALGGTVTLQLGYPFA	114
Db	61	-----VLKRPAGSHPSRWAGMGRLLLSVQLHDSGNYSYRA-GRPAGTVHLLVDVPPE	115
QY	115	RPVVSC--QAADYENFSCWSPSQISGLPTRYLTYSRKKTVLGADSORRSPSTG--PWPC--	170
Db	116	EPQLSCFRKSPLSNVVCEWGPSTPSLTT-----KAVLLYRKFNQSPAEFDQPCQY	167
QY	171	--PDQPLGAARCYVHGAEFWQSYRINTEVNPGLGAS--TRLLDVSLOSILRPPPOGLRYVE	227
Db	168	SOESQKESCQLAVPEGDS--SFIVSMCVASSVGSFKSTQTFQGGCIIQLQPPANITVT	225
QY	228	SVPGYPRRLRASWITYPASWPCQPHFLKFRLOYRPAQHFAWSTVEPAGLEE--VITDAVA	285
Db	226	AVARNPRLSVTWDQPHSMN--SSFYRLRFRFLRYRAERSKTFETTMWKDLQHHCYIHDAWS	284
QY	286	GLPHAVRVSARDLDACTWTQSWEPAGWPTSTCIPEKIPANGOLHTQEPVEPQVDSRAP	345
Db	285	GLRHVQLRAQEEFGQGEWSENPAGWTPWTES--RSSPAENEVSTPMELLDPCGYISP	342
QY	346	PRPSLQPH	353
Db	343	ESPVVQLH	350

```

RESULT 4
US-09-935-868-24
; Sequence 24, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-935-868-24

```

```

Qy 344 --APRPSLOPHRLLD 358
    ||  |  |||
Db 333 GGAPSGAQL-----LLD 345

RESULT 5
US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match 14.5%; Score 329.5; DB 9; Length 360;
Best Local Similarity 29.2%; Pred. No. 4.8e-15;
Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

Qy 5 CSGLSRVLVAVATYALVASSPFCPOAGPPGVQYQCPGRSVKLCPCPGVTAGD--PVSWFRD 62
Db 6 CALLAALLAAPGAAL--APRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW--- 60

Qy 63 GEPKLLGGPD-----SGLGHELVLAAQADSTDEGTYICOTLDGALGGTTLQOLGYPPA 114
Db 61 ----VLRRKPAAGSHPSRWAGMRLLRSVOLHDSGNYSCYRA-GRPAGTVHLLVDVPPE 115

Qy 115 RPVVSQ-QAADYENFSCWSPQISGLPTRYLTYSRKTKTVLGADSQRRSPSTG-PWPC-- 170
Db 116 EPQLSCFRKSPLSNVVCWGPSTPSLTT-----KAVLLVRKFQNSPAEDFQPCQY 167

Qy 171 --PODPLGAARCVVHGAEFWISQYINTEVNPLGAS-TRLLDVSLSQILTRPDPPOGLRVE 227
Db 168 SQESQKFSQCLAVPEGDS--SFYIVSMCVASSVSGSKFSKTQTFQCGGTLQPDPPANITVT 225

Qy 228 SVPQYPRRLRASWTYPASNPCCPHFLKLFRLQYRPAQHPAWSTVEPAGLEE--VITDAVA 285
Db 226 AVARNPRLSVTQDPHSHWN--SSFYRFLERYRAERKSTFTTVMVKDLQHHCVIHDWS 284

Qy 286 GLPHAVRSARDELDACTWTWSPSEANGTFTSTGIPKEIPAWGOLHTQPEVEPOQVDSAP 345
Db 285 GLRHVVQLRAQEEPGGESEWSEPEANGTPWTES-----RSPPAENEVSFPMQ 332

Qy 346 PRPSLQPHRLLDHRDSVEQVAV 368
Db 333 ALTTNKDDDNIL-PRDSANATSL 354

RESULT 6
US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8

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; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

Query Match      14.5%; Score 329.5; DB 9; Length 592;
Best Local Similarity 29.2%; Pred. No. 8.4e-15;
Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

Qy  5  CSGLSRVLVAVATALVASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGD--PVSWFRD 62
Db  1  : : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db  6  CALLAALLAAPGAAL--APRCPAQAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW-- 60
Qy  63  GEPKLLOGPD-----SGLGHELVLQAQADSTDEGTTCOTLDGALGGTTLQLGYPPA 114
Db  1  : : : : | : | : | | | | | | | | | | | | | | | | | | |
Db  61  ---VLRKPAAGSHPSRWAGMRLLRSVLHDSGNVSCYRA--GRPAGTVHLLVDVPPE 115
Qy  115  RPVYSC--QAADYENFSCWSPQSISGLPTRYLTYSRKTKTVLGADSQRRSPSTG--PWPC-- 170
Db  1  : : : : | : | : | | | | | | | | | | | | | | | | | | |
Db  116  EPQLSCFRKSPLSNVNCGWGRSPSLTT-----KAVLLVRKFNQSPAEDFOEPCQY 167
Qy  171  --PDPLGAARCVVHGAEFWQYRINTEVNPGLGAS--TRLLDSVLSQILRPDPPOGLRVE 227
Db  1  : : : : | : | : : : | : : : : | : | | | | | | | | | |
Db  168  SQESQKSCQLAVPEGDS--SFYIVSMCVASSVSGSKFTQTFOCGILQDPDPANITVT 225
Qy  228  SVPGYPRRLRASWTYPASWPCQPHFLKFLQYRPAQHPAWSTVEPAGLEE--VITDAVA 285
Db  1  : : | | : | | | | | | | | | | | | | | | | | | | | |
Db  226  AVARNRWLSVTWQDPHSWN--SSFYRLRFELRYRAERSKFTTTMMVKDLQHHCVIHDAWS 284
Qy  286  GLPHAVRYSAARDFLDAGTWTSWSPANGTPTSTGTIPKEIPAWGQLHTQPEVPOVDSPAP 345
Db  1  : : | : | : | | | | | | | | | | | | | | | | | | | |
Db  285  GLRHVQLRAQEFGGEWSESPAMGTPTWES-----RSPFAENEVSTPMQ 332
Qy  346  PRPSLOPHPRLLDHRDSVEQVAV 368
Db  1  : : : : | | | | | | | | | | | | | | | | | | | |
Db  333  ALTNNKDDNLL-PRDSANATSL 354

RESULT 7
US-09-935-868-16
; Sequence 16, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-16

Query Match      13.8%; Score 315; DB 9; Length 315;
Best Local Similarity 31.0%; Pred. No. 3.8e-14;
Matches 102; Conservative 38; Mismatches 149; Indels 40; Gaps 13;

Qy  5  CSGLSRVLVAVATALVASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGD--PVSWFRD 62
Db  1  : : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db  6  CALLAALLAAPGAAL--APRCPAQAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW-- 60
Qy  63  GEPKLLOGPD-----SGLGHELVLQAQADSTDEGTTCOTLDGALGGTTLQLGYPPA 114
Db  1  : : : : | : | : | | | | | | | | | | | | | | | | | | |
Db  61  ---VLRKPAAGSHPSRWAGMRLLRSVLHDSGNVSCYRA--GRPAGTVHLLVDVPPE 115
Qy  115  RPVYSC--QAADYENFSCWSPQSISGLPTRYLTYSRKTKTVLGADSQRRSPSTG--PWPC-- 170
Db  1  : : : : | : | : | | | | | | | | | | | | | | | | | | |
Db  116  EPQLSCFRKSPLSNVNCGWGRSPSLTT-----KAVLLVRKFNQSPAEDFOEPCQY 167

```

APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Pfanz, Stefan
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
FILE REFERENCE: DX01040K2
CURRENT APPLICATION NUMBER: US/09/791,497
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/627,897
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/146,581
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/147,763
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 229
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-497-12

Query Match 11.2%; Score 255.5; DB 9; Length 229;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;
QY 94 COTLDGALGGTTLQLGVPAPR---PVVSCQAADYE-NFSCCTWS--PSQISGLPTRYLTS 147
DB 15 CPFCGRKG-----PPAALTLPVQCRASTRPIADCSWTLPAPNSTSPVSFTAT 65
QY 148 YRKKTVLGADSORSPSTGPNPCQDPLGAARCVVHGAEFWSQ--YRINVTVEVNPFGAST 205
DB 66 YR---LGMARGHs-----WPCLOQTPTSTCTTIDVQLFSMAFPVVLNVTAVHPWGSS 116
QY 206 RLIDVSLQSLRPDPQGLRVESVPGYPRRLRASVTYPASWPCQPHFLKFLQRYRPAQH 265
DB 117 SVFPFTEHIIKPDPEGVRLS--PLAEHVQVQVEPPGSGWPFPEIFSLKYWIRYKROGA 174
QY 266 PAWSTVEPAGLEVTIDVAGLPHUA---VRVSARDFLDAGTWTSTWSPAEWGTPTSG 318
DB 175 ARFHRVGPIEATSFILRAVR--PRARYVQVAAQDLTDYGELSDWSLPATATMSLG 228

RESULT 10
US-09-880-578-27
Sequence 27, Application US/09880578
Patent No. US20020045733A1

GENERAL INFORMATION:
APPLICANT: Lok, Si
Presnell, Scott R.
Jelmeberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
Adams, Robyn L.
Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-880-578-27

Query Match 9.3%; Score 212.5; DB 10; Length 389;
Best Local Similarity 23.8%; Pred. No. 3e-07;
Matches 89; Conservative 54; Mismatches 136; Indels 95; Gaps 19;
QY 17 TALVSASSPCQAWGPPGVGYGPGRSVKLCC-----PGVTAGDPVSWFRDGE---PKL 67
DB 3 TAVISPDQPTLLI-----GSSLLATCSVHGDPGATA-EGLYWTLNGRRLLPPEL 50
QY 68 LOGPSGGLGHELVLAQAD-----STDEGTYICQTLGALGGTTLQLGYPARPV-VSCQ 121
DB 51 SRVLNAS---LALALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPVNISCW 107
QY 122 ADYENFSCWTSFSPQ--ISGLPTRYLTSYRKKTIVLGADSORSPSTGPNPC--PODPLCA 177
DB 108 SKNMKDLTCRWTPGAGHGETFLHTNYSLSKYLKRWYGODNTCEEYHTVGPCHSHIPKD----- 163
QY 178 ARCVVHGAEFWSQYRINVTVEVNPGLAS--TRLLDVSLSQSLRPDPQGLRVESVPGYPRRL 236
DB 164 -----LALFPYELWEATNRLGSSRSDVLTLDLDVVTDDPPDPVHVRVGGLEDQL 216
QY 237 RASWTYPASWPCQPHFL--KFRQYRPAQHPAWSTVEP-----AGLEEVITDAVA 285
DB 217 SVRWSP---PALKDFLFOAKYQIRYRVESVDWKVDDVDSNQTSCRLAGLK-----P 266
QY 286 GLPHAVRVVSARDF-----LDAGTWTWS-PEA-----WCTPSTGTI 320
DB 267 GTVYFVQVRCNPFYIGYSGKAGIWSHPTAASTPRSRPGRPGGACPRGGEPSGPV 326
QY 321 PKEIP---AWGOLH 331
DB 327 RRELKQFLGWLKX 340

RESULT 11
US-09-880-578-24
Sequence 24, Application US/09880578
Patent No. US20020045733A1
GENERAL INFORMATION:
APPLICANT: Lok, Si
Presnell, Scott R.
Jelmeberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
Adams, Robyn L.
Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA

```
;
;
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
;
; US-09-880-578-24
;
; Query Match          9.3%; Score 211.5; DB 10; Length 389;
; Best Local Similarity 23.8%; Pred. No. 3.5e-07;
; Matches 89; Conservative 53; Mismatches 137; Indels 95; Gaps 19;
;
; QY 17 TALVSASPCQAWPGVQVQGPGRSVKLC-----PGVTAGDPVSWFRDGE---PKL 67
;   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 3 TAVISPDQPTLLI-----GSSLLATCSVHGDPGPGATA-EGLYWTNLNGRRLPPEL 50
;
; QY 68 LOGPDSGLGHELVLAQAD-----STDEGTYICQTLDGALGTVTLQLYGPPARPV-VSCQ 121
;   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 51 SRVLNAS---TLALANLNGSRORSNDLVCHARDGSILAGSCLYVGLPEKPVNISCW 107
;
; QY 122 AADYENFSCWSPSQ--ISGLPTRYLTSYRKKTVLGADSORRSPSTGPWPC--PQDPLGA 177
;   : : : : | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 108 SKNMKDLTCRWTPGSHGETFLHTNYSKYLKWYGQDTCCEEYHTVGHPSCHIPKD--- 163
;
; QY 178 ARCVMHGAEFWSQYRINVTENVPLG-ASTRLLDVLSQILRPDPQGLRVESVPGYPRRL 236
;   : : | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 164 -----LALFTPYEIWVEATNRLGSARSVDLTLDILDVVTTPDPPDVHVSRVGGLEDQL 216
;
; QY 237 RASWTYPASWPCQPHFL--KFRLOYRPAQHPAMSTVEP-----AGLEEVITDAVA 285
;   | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 217 SVRWSP---PALKDFLFQAKYQIRYRVESVDWKVVDVSNQTSCLAGLK-----p 266
;
; QY 286 GLPHAVRVSARDF-----LDAGTWSTWS-PEA-----WGTPSTGTI 320
;   | : | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 267 GTVYFVQVRCNPFGIYGSKKAGIWSNHSHTAASPRSRPGGGACPRGGEPSSGPV 326
;
; QY 321 PKEIP---ANGQLH 331
;   : | : | | |
; Db 327 RRELKQFLGLWKKH 340
;
; RESULT 12
; US-09-880-578-29
; Sequence 29, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelnberg, Anna C.
; Gilbert, Teresa
```

```
;
;
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
;
; US-09-880-578-29
;
; Query Match          9.3%; Score 211.5; DB 10; Length 389;
; Best Local Similarity 24.1%; Pred. No. 3.5e-07;
; Matches 90; Conservative 52; Mismatches 137; Indels 95; Gaps 19;
;
; QY 17 TALVSASPCQAWPGVQVQGPGRSVKLC-----PGVTAGDPVSWFRDGE---PKL 67
;   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 3 TAVISPDQPTLLI-----GSSLLATCSVHGDPGPGATA-EGLYWTNLNGRRLPPEL 50
;
; QY 68 LOGPDSGLGHELVLAQAD-----STDEGTYICQTLDGALGTVTLQLYGPPARPV-VSCQ 121
;   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 51 SRVLNAS---TLALANLNGSRORSNDLVCHARDGSILAGSCLYVGLPEKPVNISCW 107
;
; QY 122 AADYENFSCWSPSQ--ISGLPTRYLTSYRKKTVLGADSORRSPSTGPWPC--PQDPLGA 177
;   : : : : | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 108 SKNMKDLTCRWTPGSHGETFLHTNYSKYLKWYGQDTCCEEYHTVGHPSCHIPKD--- 163
;
; QY 178 ARCVMHGAEFWSQYRINVTENVPLG-ASTRLLDVLSQILRPDPQGLRVESVPGYPRRL 236
;   : : | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 164 -----LALFTPYEIWVEATNRLGSARSVDLTLDILDVVTTPDPPDVHVSRVGGLEDQL 216
;
; QY 237 RASWTYPASWPCQPHFL--KFRLOYRPAQHPAMSTVEP-----AGLEEVITDAVA 285
;   | | | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 217 SVRWSP---PALKDFLFQAKYQIRYRVESVDWKVVDVSNQTSCLAGLK-----p 266
;
; QY 286 GLPHAVRVSARDF-----LDAGTWSTWS-PEA-----WGTPSTGTI 320
;   | : | | | | | | | | | | | | | | | | | | | | | | | | |
; Db 267 GTVYFVQVRCNPFGIYGSKKAGIWSNHSHTAASPRSRPGGGACPRGGEPSSGPV 326
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; QY 321 PKEIP---ANGQLH 331
;   : | : | | |
; Db 327 RRELKQFLGLWKKH 340
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: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2348PIC1
: CURRENT APPLICATION NUMBER: US/09/944,413
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090

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;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020156004A1e1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020156004A1e1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; SEQ ID NO 32
;; LENGTH: 422
;; TYPE: PRT
;; ORGANISM: Homo Saplen
US-09-944-413-32

Query Match 9.3% Score 211.5; DB 9; Length 422;

Best Local Similarity 23.7%; Pred No. 3.9e-07;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

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Db 30 GAPRAGSGAHTAVISPDQPTLLI-----GSSILATCSVHGPPPGATA-EGLYWT 77
QY 61 RDGE---PKLLOGDPSGLGHELVLAQAD-----STDGTYICQLDGAALGTVTLQGY 112
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QY 113 PARPV-VSCOAADYENFSCTWSPSQ--ISGLPTRYLTSYRKKTVLGDSORRSPSTGPWP 169
Db 135 PEKPVNISCSKNNKDLTCWTPGAHGETFLHTNYSLKYLKWYQDNTCEEYHTVGP 194
QY 170 C--QDPLGAARCVVHGAEFWSQYRINVTENPLG-ASTRLDVSLSILRPDPQGLRV 226
Db 195 CHPKD-----LALFTPEIWEATNRLGARSVDVLTLDLDVVTDDPPDPVHV 243
QY 227 ESNVGPYPRRLRASWTYFASWPCQPHLL--KFRLOYRPAQHPANSTVEP-----AG 275
Db 244 SRVGLEDQLSVRWVSP---PALKDLFQAKYQIRYVEDSDVMKVVDDVSNQTSCLAG 300
QY 276 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWSTWS-PEA-----311
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Db 354 RGGPESSGPVRRLEKQFLGLWKKH 377
RESULT 15
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;; Sequence 32, Application US/09944403
;; Patent No. US20020165143A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin
;; APPLICANT: Botstein, David
;; APPLICANT: Eaton, Dan

;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Kljavin, Ivar
;; APPLICANT: Napier, Mary
;; APPLICANT: Roy, Margaret
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/944,403
;; PRIOR FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
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;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
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;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
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;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
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;; PRIOR FILING DATE: December 16, 1998
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;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
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;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020165143A1e1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313

;; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 32
;; LENGTH: 422
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-403-32

Query Match 9.3%; Score 211.5; DB 9; Length 422;
Best Local Similarity 23.7%; Pred. No. 3.9e-07;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

Qy 7 GLSRVLVAVATVAVASSPCQAWPGVQVQGPGRSVKLC-----PGVTAGDPVSWF 60
Db 30 GAPRAGSAHTAVISPDPTLLI-----GSSLLATCSVHGDPGATA-EGLYWT 77

Qy 61 RDGE---PKLQGPSGLGHELVLAQAD-----STDEGTICQTLDGALGGTVTTLQLGYP 112
Db 78 LNGRLPPPELSRVLNAS---TLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 134

Qy 113 PARPV-VSCQAADYENFCTWSPSQ--ISGLPTRYLTYSRKKTVLGADSORRSPSTGPWP 169
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Db 354 RGEPSGPGVRRELKQFLGWLKKH 377

Search completed: January 17, 2003, 19:40:18
Job time : 17 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:36:45 ; Search time 18 Seconds
(without alignments)
689.804 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27	232	10.2	386	6	5171840-5

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ALIGNMENTS

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; Sequence 2, Application US/09151102
; Patent No. 6274547
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151,102
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-151-102-2

Query Match 100.0%; Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 421 NL 422

RESULT 2

US-08-929-846-2
; Sequence 2, Application US/08929846
; Patent No. 6350855
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/929,846
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5252
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-929-846-2

Query Match 100.0%; Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQOPGRSVKLCPCGVTAGDPVSWF 60
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QY 181 VVHGAEFWSQYRINVTENPLGASTRLLDVLSQTLRDPQGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENPLGASTRLLDVLSQTLRDPQGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLVEEITDAVAGLPHAVRVVSARDFLD 300
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Db 301 AGTWSTWSPCAWGTPTGTIPKEIPANGQLHTQPEVEPQVDSAPPRLSLQPHPRLLDHR 360
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Db 361 DSVEQVAVLASGLTSLFGLVAGALALGLWLRLRRGGKDGSPKPGFLASVIPVDRRPGAP 420
QY 421 NL 422
Db 421 NL 422

RESULT 3
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; Sequence 5, Application US/08702665A
; Patent No. 6274708
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,665A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 10296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 203 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-665A-5

Query Match 99.2%; Score 2257.5; DB 4; Length 423;
Best Local Similarity 99.5%; Pred. No. 3.5e-172;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPSVWF 60
DB 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPSVWF 60
QY 61 RDGEPLKLGPPDSGLGHELVLAQADSTDEGTTCQTLDGALGCTVTLOLGYPPARPVWSC 120
DB 61 RDGEPLKLGPPDSGLGHELVLAQADSTDEGTTCQTLDGALGCTVTLOLGYPPARPVWSC 120
QY 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPPCQDPLGAARC 180
DB 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPPCQDPLGAARC 180
QY 181 VHGAEFWQYRINVTENVPL-GASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRAS 239
DB 181 VHGAEFWQYRINVTENVPLGGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRAS 240
QY 240 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDEL 299
DB 241 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDEL 300
QY 300 DAGTWTWSPEAWGTSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRLLDH 359
DB 301 DAGTWTWSPEAWGTSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRLLDH 360
QY 360 RDSVEQVAVLASGLISFLGLVAGALALGLWLRGGKDGSPKPGFGLASVIVDRRPGA 419
DB 361 RDSVEQVAVLASGLISFLGLVAGALALGLWLRGGKDGSPKPGFGLASVIVDRRPGA 420
QY 420 PNL 422
DB 421 PNL 423

RESULT 4

US-08-702-665A-3
Sequence 3, Application US/08702665A
Patent No. 6274708
GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/702,665A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 10296
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
TELEX: 203 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-665A-3

Query Match 83.4%; Score 1897; DB 4; Length 432;
Best Local Similarity 83.5%; Pred. No. 1.9e-143;
Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;
QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPSVWF 60
DB 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPSVWF 60
QY 61 RDGEPLKLGPPDSGLGHELVLAQADSTDEGTTCQTLDGALGCTVTLOLGYPPARPVWSC 120
DB 61 RDGEPLKLGPPDSGLGHELVLAQADSTDEGTTCQTLDGALGCTVTLOLGYPPARPVWSC 120
QY 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPPCQDPLGAARC 180
DB 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTLPGAESQRESPTGPPCQDPLEASRC 180
QY 181 VHGAEFWQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRASW 240
DB 181 VHGAEFWQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLHAW 240
QY 241 TYPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
DB 241 TYPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
QY 301 AGTWTWSPEAWGTSTGTIPKEIPAWQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLD 358
DB 301 AGTWTWSPEAWGTSTGTIPKEIPAWQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLD 360
QY 359 HRDSVEQVAVLASGLISFLGLVAGALALGLWLRGGKDGSPKPGFGLASVIVDRRPG 418
DB 361 HRDPLEQVAVLASGLISFLGLVAGALALGLWLRGGKDGSPKPGFGLASVIVDRLPG 420
QY 419 APNL 422
DB 421 IPNL 424

RESULT 5

US-09-151-102-4
Sequence 4, Application US/09151102
Patent No. 6274547
GENERAL INFORMATION:
APPLICANT: Tobin, James
TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,102
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,584

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;
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-151-102-4

Query Match      80.5%; Score 1831; DB 4; Length 441;
Best Local Similarity 83.1%; Pred. No. 3.6e-138;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;

QY 16 ATALVSASSPCQAWGPPGVQYQPGQSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSDL 75
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Db 25 ATALVSSSPCQAWGPPGVQYQPGQSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSDL 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 GHELVLQAQADSDTEGYICQTLGALGGTVTLQGYPPARPVVSQAADYENFSCTWSPS 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 GHRLVLAQVDSDEGYVQCOTLDGVSGGMVTLKLGFPFAPPEVSCQAVDYENFSCTWSPG 144
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 136 QISGLPTRYLTYSRKKTVLGADSQRRSPSTGPPCPQDPLGAARCVVHGAEFWSQYRINV 195
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 QVSGLPTRYLTYSRKKTLPGAESQRESPTGPPCPQDPLGAARCVVHGAEFWSQYRINV 204
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 196 TEVNLGASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 TEVNLGASTCLLDVRLQSLRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 256 FRLOYPQAHPAWSTVEPAGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSTWSPAWGTP 315
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWSPEAWGTP 324
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 316 STGTIPKEIPAWQLHTQ--PEVEPQVDSAPPRLSLOPHRLDHRDSVEQAVLASLG 373
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Db 325 STGPLQDEIPDWSQGHGOOLEAVQAQEDSPAPARSLQDPDRPLDHRDPLEQVAVLASLG 384
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

QY 374 ILSFGLVAGALALGLWLRRLRRGGKGPFGFLASVIPVDRRPGAPNL 422
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 385 IFSCGLAVGALALGLWLRRLRRSGKDGKPKGCLLAPMIPVEKLPGLPINL 433
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RESULT 6
US-09-929-846-4
; Sequence 4, Application US/08929846
; Patent No. 6350855
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,846
```

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;
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-929-846-4

Query Match      80.5%; Score 1831; DB 4; Length 441;
Best Local Similarity 83.1%; Pred. No. 3.6e-138;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;

QY 16 ATALVSASSPCQAWGPPGVQYQPGQSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSDL 75
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 ATALVSSSPCQAWGPPGVQYQPGQSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSDL 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 GHELVLQAQADSDTEGYICQTLGALGGTVTLQGYPPARPVVSQAADYENFSCTWSPS 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 GHRLVLAQVDSDEGYVQCOTLDGVSGGMVTLKLGFPFAPPEVSCQAVDYENFSCTWSPG 144
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 136 QISGLPTRYLTYSRKKTVLGADSQRRSPSTGPPCPQDPLGAARCVVHGAEFWSQYRINV 195
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Db 145 QVSGLPTRYLTYSRKKTLPGAESQRESPTGPPCPQDPLGAARCVVHGAEFWSQYRINV 204
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QY 196 TEVNLGASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 TEVNLGASTCLLDVRLQSLRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 256 FRLOYPQAHPAWSTVEPAGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSTWSPAWGTP 315
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWSPEAWGTP 324
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 316 STGTIPKEIPAWQLHTQ--PEVEPQVDSAPPRLSLOPHRLDHRDSVEQAVLASLG 373
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 325 STGPLQDEIPDWSQGHGOOLEAVQAQEDSPAPARSLQDPDRPLDHRDPLEQVAVLASLG 384
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

QY 374 ILSFGLVAGALALGLWLRRLRRGGKGPFGFLASVIPVDRRPGAPNL 422
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 385 IFSCGLAVGALALGLWLRRLRRSGKDGKPKGCLLAPMIPVEKLPGLPINL 433
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RESULT 7
US-09-211-590-2
; Sequence 2, Application US/09211590
; Patent No. 6316206
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/211,590
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-211-590-2

Query Match 16.8%; Score 382; DB 4; Length 372;
Best Local Similarity 30.1%; Pred. No. 8.6e-23;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALYSASSPCQANGPGVQYQGRSVKLCPCPGVTAGDPVSWFRDGEPLKLOGP 71
DB 12 VLAAAAYVYQHRSPQE--APHVQYERLGSVDTLPCGTANWDAAVTRVNGTD---LAP 66
QY 72 DSGHGLHVLQAADSTDEGTICQTLDG-ALGCTVTLQLGYPPARPVVSCQAADY-ENFS 129
DB 67 DLLNGSQLVHLGLHGLSGLYACFHRDSWHLRHQVLLHVLGLPPREPVLSCRSNTYKGFY 126
QY 130 CWTSPSQISGLPT-RYLTYSRKTKTVLGADSRSPSTGPPCPQDPDLGAARCVVHGAEFW 188
DB 127 CSWH-----LPTPTIPNTFNTVTLHGSK-----IMVCEKDPALKNRCHIRYMHLF 172
QY 189 S--OYRINTEVNPLGASTRLDVSILRPPDPOGLRVESVPGYPRRLRASWTYPASW 246
DB 173 STIKYKVSISVSNALGNATAITFDEFTIVKPPENNVARVPSPNRRLEVTWQTPSTW 232
QY 247 PCQPHFLKFRLOYRPAQHPAWSTVEPA-GLEEVITDVAAGLPHAVRVSAARDFLDAGTWS 305
DB 233 PDPEFPKFLFRYRPLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKD-NEIGTWS 291
QY 306 TWSPEAWGTPSTGTIPKEIPAWQLHTQPEVEQVDSAPPRLSLQPHPLLDHRDSVEQ 365
DB 292 DWSVAHAATPWTEE-PRHLTTEAQ--AAETTTTSTSLAPP-----PTTKICD----- 336
QY 366 VAVLASIGILSFLGVAGALALGLWLRRLRGKGDKGPKGFLASV 410
DB 337 -----PGEL-----GSGGGPSAPFLVSV 354

RESULT 8
US-07-865-878A-4
Sequence 4, Application US/07865878A
Patent No. 5332672
GENERAL INFORMATION:
APPLICANT: Yancopoulos, George D. et al.
TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
Factor/Receptor Complex
NUMBER OF INVENTIONS: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/865,878A
FILING DATE: 19911202
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/801/562
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-082
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-865-878A-4

Query Match 16.7%; Score 379; DB 1; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALYSASSPCQANGPGVQYQGRSVKLCPCPGVTAGDPVSWFRDGEPLKLOGP 71
DB 12 VLAAAAYVYQHRSPQE--APHVQYERLGSVDTLPCGTANWDAAVTRVNGTD---LAP 66
QY 72 DSGHGLHVLQAADSTDEGTICQTLDG-ALGCTVTLQLGYPPARPVVSCQAADY-ENFS 129
DB 67 DLLNGSQLVHLGLHGLSGLYACFHRDSWHLRHQVLLHVLGLPPREPVLSCRSNTYKGFY 126
QY 130 CWTSPSQISGLPT-RYLTYSRKTKTVLGADSRSPSTGPPCPQDPDLGAARCVVHGAEFW 188
DB 127 CSWH-----LPTPTIPNTFNTVTLHGSK-----IMVCEKDPALKNRCHIRYMHLF 172
QY 189 S--OYRINTEVNPLGASTRLDVSILRPPDPOGLRVESVPGYPRRLRASWTYPASW 246
DB 173 STIKYKVSISVSNALGNATAITFDEFTIVKPPENNVARVPSPNRRLEVTWQTPSTW 232
QY 247 PCQPHFLKFRLOYRPAQHPAWSTVEPA-GLEEVITDVAAGLPHAVRVSAARDFLDAGTWS 305
DB 233 PDPEFPKFLFRYRPLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKD-NEIGTWS 291
QY 306 TWSPEAWGTPSTGTIPKEIPAWQLHTQPEVEQVDSAPPRLSLQPHPLLDHRDSVEQ 365
DB 292 DWSVAHAATPWTEE-PRHLTTEAQ--AAETTTTSTSLAPP-----PTTKICD----- 336
QY 366 VAVLASIGILSFLGVAGALALGLWLRRLRGKGDKGPKGFLASV 410
DB 337 -----PGEL-----GSGGGPSAPFLVSV 354

RESULT 9
US-07-676-647-2
Sequence 2, Application US/07676647
Patent No. 5426177
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.


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Db      292 DWSVAATATPTEE-PRLHTEAQ--AAETTTTSTSLAPP-----PTTKICD-
Qy      366 VAVLASLGILSFGLVAGALALGLWLRGRGKDGSPKPGFLASV 410
Db      337 -----PGEL-----GSGGGPCAPFLVSV 354

RESULT 12
US-08-585-258-2
; Sequence 2, Application US/08585258
; Patent No. 5892003
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,258
; FILING DATE: 11-JAN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/001,904
; FILING DATE:
; APPLICATION NUMBER: US/07/700,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-585-258-2

Query Match 16.7%; Score 379; DB 2; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps

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Db 173 STIKYKVSISVSNALGHNNATAITFDEFTIVKDPDENNVAVRVPSPNPRLEVTWOTPTSTW 232
QY 247 PCQPHFLKFRLOYPQAHPAWSTVEPA-GLEEVITDAVAGLPHAVRVARSARDFLDAGTWS 305
Db 233 PDPESEFPLAFRLRYRLIILDOHQHVELSDGTAHTIIDAVAGKEYIIQVAAKD-NEIGTWS 291
QY 306 TWSPEAWGTPTGTIPKEIPANGQLHTQPEVEPQVDSAPPSPRPSLQPHRLLDHRDSVQ 365
Db 292 DMSVAHAHATPTEE-PRHLTTEAQ--AETTTSTTSLAPP-----PTTKICD----- 336
QY 366 VAVLASLGLSLFLGVLVAGALALGLWLRRLRGKDGSPKPGFLASV 410
Db 337 -----PGEL-----GSGGPCAPFLVSV 354

RESULT 13
US-08-603-010-4
; Sequence 4, Application US/08603010
; Patent No. 5955290
; GENERAL INFORMATION:
; APPLICANT: Yancopoulos, George D. et al.
; TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
; TITLE OF INVENTION: Factor/Receptor Complex
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,010
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/118,968
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: US 07/801,562
; FILING DATE: 02-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-603-010-4

Query Match 16.7%; Score 379; DB 2; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALVSASSPCQAWGPGVQYQOPGRSVKLCPCGVTAGDVPVSWFRDGEPKLLOGP 71
Db 12 VLAAAAVVVYQRRHSPOE--APHVQYERLGSVDVTLPCGTANWDAAVTWRVNGTD---LAP 66
QY 72 DSGLGHELVLQAADSTDEGTTCQTLDC-ALGGTVTQLGYPARPYPVYSCQAADY-ENFS 129
Db 67 DLLNGSQLVLHGLHLSGLTACFHRDSWHLRHQVLLHVLGPPREPVLSCRSNTYPKGFY 126

QY 130 CTWSPSQISGLPT-RVLTYSRKTKTVLGDASQRRSPSTGPWPQDPDLGAARCVVHGAEFW 188
Db 127 CSMH-----LPTPTYPNTFNVTVLHSGK-----IMVCEKDPALKNRCHIRYWHLP 172
QY 189 S--QYRINVTENVPLGASTRLLDVSLQSLRDPDPOGLRVESVPGYPRRLRASWTYPASW 246
Db 173 STIKYKVSISVSNALGHNNATAITFDEFTIVKDPDENNVAVRVPSPNPRLEVTWOTPTSTW 232
QY 247 PCQPHFLKFRLOYPQAHPAWSTVEPA-GLEEVITDAVAGLPHAVRVARSARDFLDAGTWS 305
Db 233 PDPESEFPLAFRLRYRLIILDOHQHVELSDGTAHTIIDAVAGKEYIIQVAAKD-NEIGTWS 291
QY 306 TWSPEAWGTPTGTIPKEIPANGQLHTQPEVEPQVDSAPPSPRPSLQPHRLLDHRDSVQ 365
Db 292 DMSVAHAHATPTEE-PRHLTTEAQ--AETTTSTTSLAPP-----PTTKICD----- 336
QY 366 VAVLASLGLSLFLGVLVAGALALGLWLRRLRGKDGSPKPGFLASV 410
Db 337 -----PGEL-----GSGGPCAPFLVSV 354

RESULT 14
PCT-US91-03896-2
; Sequence 2, Application PC/TUS9103896
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03896
; FILING DATE: 19910603
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-065-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US91-03896-2

Query Match 16.7%; Score 379; DB 5; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALVSASSPCQAWGPGVQYQOPGRSVKLCPCGVTAGDVPVSWFRDGEPKLLOGP 71
Db 12 VLAAAAVVVYQRRHSPOE--APHVQYERLGSVDVTLPCGTANWDAAVTWRVNGTD---LAP 66
QY 72 DSGLGHELVLQAADSTDEGTTCQTLDC-ALGGTVTQLGYPARPYPVYSCQAADY-ENFS 129

Db 67 DLLNGSLVHLGHLGSLVACFRDSDHMLRHQVLLHVGLPPRPBVLSCRSNTYPKGFY 126
QY 130 CTWSPQISGLPT-RYLTYSRKKTVLGADSORRSPSTGPWPQDPQPLGAARCVVHGAEFW 188
Db 127 CSWH-----LPTPYIPNTFNTVTLHSGK-----IMWCEKDPALKNRCHIRYMHLF 172
QY 189 S--QYRINVTENPLGASTRLLDVLSQSLRPDPPOGLRVESVPGYPRRLRASWTYPASW 246
Db 173 SPIKVKVTSVSNALGHNAITATFDEFTIVKPDPPENVVAVRPNRRLEVTWQTPSTW 232
QY 247 PCQPHELKFLRQYRPAQHPASTVEPA-GLIEVLTDAVAGLPHAVRVSARDFLDAGTWS 305
Db 233 PDPEFPLKFLURYLPLLDOMHVELSDGTAHTITDAYAGKEYTIQVAKD-NEIGTWS 291
QY 306 TWSPEAWGTPTGTIPKEIPAWGQLHTQPEVEPQVDSPPAPRPSLQPHRLLDHRDSVEQ 365
Db 292 DMSVAHAATPWEE-PRHLTTEAQ-AAETTTSTTSSLAPP-----PTTKICD----- 336
QY 366 VAVLASLGLSLVAGALALGLWLRLRRGGKDGSPKPGFLASV 410
Db 337 -----PGEL-----GSGGGPCAPFLVSV 354

RESULT 15

US-08-795-473B-5

; Sequence 5, Application US/08795473B

; Patent No. 6217858

; GENERAL INFORMATION:

; APPLICANT: Galun, Eithan

; APPLICANT: Nahot, Orit

; APPLICANT: Blum, Herbert E.

; TITLE OF INVENTION: A Pharmaceutical Composition for Treating

; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Davidson, Davidson and Kappel, LLC

; STREET: 1140 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS-DOS EDITOR

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795.473B

; FILING DATE: 11-FEB-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Davidson, Clifford M.

; REGISTRATION NUMBER: 32,728

; REFERENCE/DOCKET NUMBER: 963.1007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)-997-1028

; TELEFAX: (212)-997-1037

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 468 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

US-08-795-473B-5

Query Match 15.8%; Score 360; DB 4; Length 468;

Best Local Similarity 28.4%; Pred. NO. 6.6e-21;

Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

QY 1 MSSCSGLSLRVAVATLVASASSPCQAWGPPGYQGPGRSVKLCPCGVTAGD--PVS 58

Db 2 LAVGALLAALLIAPGAAL--APRCPAQEVARGVITSLPGDSVTLTCPGVEPEDNATVH 59

QY 59 WFRDGEPKLQGPD-----SGLGHELVLAQAADSTDEGTIVICQTLGALGGTVTTLQIG 110

Db 60 W-----VLRKPAAGSHPSRWAGMGRLLLRVOLHDSGNYSYRA-GRPAGTVHLLVD 111
QY 111 YPPARPVVSC-QAADYENFSCWTWSPQISGLPTRLTYSRKKTVLGADSORRSPSTG-PW 168
Db 112 VPPEPQLSCFRKSPLSNVVCEWGRSTPSLT-----KAVLLVRKFQNSPAEDFOE 163
QY 169 PC-----PQDPLGAARCVVHGAEFWSQYRINVTENVPLGAS-TRLLDVSLSQSLRDPDPQ 223
Db 164 PCQYSESQKFSQCOLAVPEGDS--SFYIVSMCVASSVSGSKFTQTFQCGGILQDPDPAN 221
QY 224 LRVESVPGYPRRLRASWTYPASWPCQPHLLKFRLOYRPAQHPAWSTVEPAGLEE--VIT 281
Db 222 ITVTAVARNPRWLSVTQDQPHSWN--SSEYRLRFLRYRAERSKTTTWMVKDLQHHCVIH 280
QY 282 DAVAGLPHAVRVSARDFLDAGTWTWSPAMGTPTGTIPKEIPAWGQLHTQPEVEPOVD 341
Db 281 DAWSLRHVVQLRAQDEEFGQGEWSEWSPAMGTPTWES-----RSPPAENEVS 328
QY 342 SPAPRPSLQPHRLLDHRDSVEQVAV-----LASLGLISFLGLVAGALALG----- 388
Db 329 TPMQALTTNKDDNLL-FRDSANATSLPVQDSSSVPLPTFL-VAGSLAFGLLCLIAIVL 386
QY 389 -----LW-LRLRRGGKDGSPKPGFLASVIPVDRRP 417
Db 387 RFKKTWKLRLALKEGKTSMHPPYSGLQLVPERPRP 420

Search completed: January 17, 2003, 19:39:29

Job time : 21 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:33:55 ; Search time 41 seconds

(without alignments)
1371.506 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSLGRVLVAVATALV.....KPGFLASVIVDRRPGPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2275	100.0	422	17	AA990900 Human interleukin-
2	2275	100.0	422	22	AA936654 Human IL-11 recept
3	2275	100.0	422	22	AAU07725 Human interleukin
4	2275	100.0	422	23	AAE14613 Human interleukin-
5	2257.5	99.2	423	17	AA92814 Human interleukin-
6	1897	83.4	432	17	AA92813 Murine interleukin
7	1871	82.2	432	22	AA936653 Mouse IL-11 recept
8	1831	80.5	441	17	AA990901 Murine Etl-2 gene
9	1831	80.5	441	22	AAU07726 Mouse Etl-2. Mus
10	1831	80.5	441	23	AAE14614 Murine Etl-2 prote

11	1680	73.8	379	21	AAV59390	Murine soluble int
12	771	33.9	257	23	ABB06126	Human NS protein s
13	395.5	17.4	460	13	AA922616	IL-6R for soluble
14	395.5	17.4	460	22	AA936656	Mouse IL-6 recepto
15	382.5	16.8	460	13	AA913318	IL-6 receptor. Mu
16	379	16.7	372	13	AA920024	Ciliary neurotroph
17	379	16.7	372	14	AA937820	Sequence of human
18	379	16.7	372	16	AA970147	Human recombinant
19	378	16.6	349	22	AA963546	Amino acid sequenc
20	363	16.0	468	17	AA988364	Interleukin-6 rece
21	360	15.8	468	10	AA990284	Sequence of a rece
22	360	15.8	468	14	AA937215	IL-6 receptor. Sy
23	360	15.8	468	22	AA936655	Human IL-6 recepto
24	351	15.4	468	10	AA90525	B cell stimulating
25	350	15.4	468	19	AA971371	Human interleukin-
26	339	14.9	1158	21	AA922205	Fusion polypeptide
27	335.5	14.7	525	18	AA936846	Human fusion polyp
28	332	14.6	1168	21	AA922204	Fusion polypeptide
29	330.5	14.5	543	20	AA903164	Chimeric sil-6R/IL
30	330	14.5	344	10	AA90528	B cell stimulating
31	330	14.5	345	21	AAV55071	SR345 protein sequ
32	329.5	14.5	360	20	AA970804	Amino acid sequenc
33	329.5	14.5	360	21	AA92199	Soluble human IL-6
34	329.5	14.5	468	21	AA921996	Human IL-6R-alpha-
35	329.5	14.5	477	21	AA92197	Human IL-6R-alpha-
36	329.5	14.5	592	20	AA970797	Human interleukin-
37	329.5	14.5	592	21	AA92185	Human IL-6R-alpha-
38	329.5	14.5	690	21	AA92195	Human IL-6R-alpha-
39	325	14.3	326	15	AA958304	Rat ciliary neuro
40	322.5	14.2	515	21	AA915404	IL-6R/IL-6 fusion
41	321	14.1	323	10	AA90527	B cell stimulating
42	316.5	13.9	1042	16	AA970122	IL8-R type 1-GP 1
43	316	13.9	325	21	AA915389	Human interleukin
44	316	13.9	325	21	AA915390	Bovine interleukin
45	315	13.8	315	20	AA970805	Amino acid sequenc

ALIGNMENTS

RESULT 1
AA990900
ID AA990900 standard; Protein; 422 AA.
XX
AC AA990900;
XX 09-OCT-1996 (first entry)
DT Human interleukin-11 receptor.
DE
DE
DE
XX
KW Interleukin-11 receptor; IL-11 receptor; antagonist; bone;
KW osteoporosis; Paget disease; myeloma.
XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Peptide	1..23
FT	Protein	/label= Sig_peptide 24..422
FT	Domain	/label= Mat_protein 24..365
FT	Region	/label= Extracellular_domain 24..111
FT	Region	/label= Ig-like_region 112..365
FT	Region	/label= Type-1-cytokine_region 366..390
FT	Domain	/label= Transmembrane_domain 391..422
FT	Domain	/label= Intracellular_domain
XX		WO9619574-A1.

PD 27-JUN-1996.
XX
XX 27-NOV-1995; 95WO-US15400.
XX
XX 22-DEC-1994; 94US-0362304.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Tobin JF;
XX
XX WPI; 1996-309588/31.
DR N-PSDB; AAT33278.
XX
XX New nucleic acid encoding human interleukin 11 receptor - and
PT related protein, antibodies, receptor antagonists, etc, useful for
PT treating and preventing loss-of bone mass
XX
XX Claim 13; Page 35-37; 54pp; English.
XX
XX Human interleukin-11 (IL-11) receptor (AAR99090) is thought to play a
CC role in the regulation of bone maturation and repair. Its amino
CC acid sequence was deduced from a cDNA clone (AAT33278) isolated from
CC a human activated peripheral blood mononuclear cell cDNA library.
CC Recombinant IL-11 receptor or its fragments, pref. amino acids
CC 24-422, 24-365 (soluble extracellular domain), 391-422, 102-422 or
CC 102-365, can be expressed in host cell systems. It is used to
CC treat/prevent loss of bone mass (e.g. osteoporosis, Paget's disease,
CC multiple myeloma or hypogonadal conditions), as well as immune
CC diseases and cancer.
XX
XX Sequence 422 AA;
XX
Query Match 100.0%; Score 2275; DB 17; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
Db 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
QY 61 RGEPLKLGPDGSLGHELVLAQADSTDEGTYICQTLDGALGCTVTLQGYPPARPVSC 120
Db 61 RGEPLKLGPDGSLGHELVLAQADSTDEGTYICQTLDGALGCTVTLQGYPPARPVSC 120
QY 121 QAADYENFSCWTSPSOISGLPTRYLYTSYRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180
Db 121 QAADYENFSCWTSPSOISGLPTRYLYTSYRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180
QY 181 VHGAEFWQYRINVTENVPLGASTRLLDVSLQSLRPDPPOGLRVESVPGYPRRLRASW 240
Db 181 VHGAEFWQYRINVTENVPLGASTRLLDVSLQSLRPDPPOGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCOPHLLKFLRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASRDFLD 300
Db 241 TYPASWPCOPHLLKFLRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASRDFLD 300
QY 301 AGTWTSWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360
Db 301 AGTWTSWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360
QY 361 DSVEQVAVLASLIGLISFLGLVAGALALGLWLRGGKDGSPKPGPLASVIVPDRPGAP 420
Db 361 DSVEQVAVLASLIGLISFLGLVAGALALGLWLRGGKDGSPKPGPLASVIVPDRPGAP 420
QY 421 NL 422
Db 421 NL 422
RESULT 2
AAB36654
ID AAB36654 standard; Protein; 422 AA.
XX

AC AAB36654;
XX
XX 13-MAR-2001 (first entry)
XX
XX Human IL-11 receptor subunit alpha protein SEQ ID NO:11.
XX
XX DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
KW immunological disorder.
XX
XX Homo sapiens.
XX
XX WO200073451-A1.
XX
XX 07-DEC-2000.
XX
XX 30-MAY-2000; 2000WO-US14867.
XX
XX 01-JUN-1999; 99US-0322913.
XX
XX (SCHE) SCHERING CORP.
XX
XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
XX
XX WPI; 2001-061536/07.
XX
XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
PT useful for regulating immune system function and for treating
PT immunological disorders -
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
CC The DCRS2 polypeptide is useful for binding ligands and for preparing
CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
CC proliferation, for diagnostic and therapeutic applications, for
CC detecting presence of their ligands and in drug screening assays. It
CC is also useful for treating conditions such as immunological disorders.
CC The present sequence represents a cytokine receptor subunit protein
CC which is given in an alignment of various cytokine receptor subunits in
CC the exemplification of the present invention.
XX
XX Sequence 422 AA;
XX
Query Match 100.0%; Score 2275; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
Db 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
QY 61 RGEPLKLGPDGSLGHELVLAQADSTDEGTYICQTLDGALGCTVTLQGYPPARPVSC 120
Db 61 RGEPLKLGPDGSLGHELVLAQADSTDEGTYICQTLDGALGCTVTLQGYPPARPVSC 120
QY 121 QAADYENFSCWTSPSOISGLPTRYLYTSYRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180
Db 121 QAADYENFSCWTSPSOISGLPTRYLYTSYRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180
QY 181 VHGAEFWQYRINVTENVPLGASTRLLDVSLQSLRPDPPOGLRVESVPGYPRRLRASW 240
Db 181 VHGAEFWQYRINVTENVPLGASTRLLDVSLQSLRPDPPOGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCOPHLLKFLRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASRDFLD 300
Db 241 TYPASWPCOPHLLKFLRQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASRDFLD 300
QY 301 AGTWTSWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360
Db 301 AGTWTSWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360

Qy 361 DSVEQAVLASLGILSLFGLVAGALGLWLRLRRGGKDGSPKPGFLASVIPVDRRPGAP 420
 Db 361 DSVEQAVLASLGILSLFGLVAGALGLWLRLRRGGKDGSPKPGFLASVIPVDRRPGAP 420

Qy 421 NL 422
 Db 421 NL 422

RESULT 3
 AAU07725
 ID AAU07725 standard; Protein; 422 AA.
 AC AAU07725;
 XX
 DT 04-DEC-2001 (first entry)
 XX Human interleukin 11 receptor, IL-11R.
 DE
 KW Human; interleukin 11 receptor; IL-11R; cytostatic; antianaemic;
 KW osteopathic; leukopaenia; bacterial infection; viral infection; anaemia;
 KW B cell deficiency; T cell deficiency; haematopoietic cell deficiency;
 KW bone marrow transplantation; immune deficiency; cancer; osteoporosis;
 KW Paget's disease; multiple myeloma; hypogonadism.
 XX
 OS Homo sapiens.
 XX
 PH Location/Qualifiers
 FT 1..22
 FT /label= Signal_peptide
 FT /note= "Alternative signal peptide"
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 FT 1..23
 FT /label= Signal_peptide
 FT /note= "Alternative signal peptide"
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 FT /label= Signal_peptide
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 FT Protein
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 FT /label= Mature_IL-11R
 FT /note= "Alternative mature protein"
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 FT /label= Immunoglobulin_like_domain
 FT Domain
 FT 24..365
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 FT claim 1, this domain may start at residue 23"
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 FT claim 1"
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 FT claim 2"
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 PN USG274547-B1.
 XX

PD 14-AUG-2001.
 XX
 PF 10-SEP-1998; 98US-0151102.
 XX
 PR 14-JUN-1996; 96US-0663584.
 PR 15-SEP-1997; 97US-0929846.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Tobin J;
 PI
 XX WPI; 2001-549157/61.
 DR N-PSDB; AAS11970.
 DR
 XX Binding inhibition of interleukin-11 to the human IL-11 receptor,
 PT useful for treatment of anaemia comprises administration of a
 PT composition containing a human IL-11R receptor protein comprising
 PT specific amino acid sequence -
 XX
 XX Claim 1; Column 19-22; 19pp; English.
 PS
 XX The invention relates to a method of inhibition binding of interleukin-11
 CC (IL-11) to the human IL-11 receptor comprises administration of a
 CC composition containing a human IL-11R receptor protein comprising an
 CC amino acid sequence of 24-365, 102-365, 24-359, or 24-345 or 24-324 amino
 CC acids of the human IL-11R protein sequence appearing as AAU07725. The
 CC method is used for inhibiting binding of IL-11 to the human IL-11
 CC receptor for the treatment of leukopaenia, bacterial and viral
 CC infections, anaemia, B cell or T cell deficiencies such as immune cell or
 CC haematopoietic cell deficiency followed by bone marrow transplantation,
 CC immune deficiency, cancer, regulation of bone maturation and repair, bone
 CC loss (including that associated with osteoporosis, post-menopausal
 CC osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
 CC disease, multiple myeloma and hypogonadal conditions). The present
 CC sequence represents human IL-11R.
 XX
 SQ Sequence 422 AA;
 Query Match 100.0%; Score 2275; DB 22; Length 422;
 Best Local Similarity 100.0%; Pred. No. 1.2e-150;
 Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCCPGVTAGDPVSWF 60
 Db 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCCPGVTAGDPVSWF 60

Qy 61 RDGEPKLLQGDPSGLGHELVLAQADSTDEGTICOTLDGALGGTTLQLGYPARPVWSC 120
 Db 61 RDGEPKLLQGDPSGLGHELVLAQADSTDEGTICOTLDGALGGTTLQLGYPARPVWSC 120

Qy 121 QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORRSPSGPMPGCPDPLGAARC 180
 Db 121 QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORRSPSGPMPGCPDPLGAARC 180

Qy 181 VVHGAEFWSQYRINVTENVPLGASTRLDVSLSQSLTRPDPPQGLRVESVPGYPRRLRASW 240
 Db 181 VVHGAEFWSQYRINVTENVPLGASTRLDVSLSQSLTRPDPPQGLRVESVPGYPRRLRASW 240

Qy 241 TYPASWPCOPHFLKFRLOYRPAQHPAWSTVEPAGLEEVIITDAVAGLHFAVRVRSARDFLD 300
 Db 241 TYPASWPCOPHFLKFRLOYRPAQHPAWSTVEPAGLEEVIITDAVAGLHFAVRVRSARDFLD 300

Qy 301 AGTWSTWSPGAWGTPTGTIPKEIPAWQLHTQPEVEFQVDSPPAPRPSLQPHRLLDHR 360
 Db 301 AGTWSTWSPGAWGTPTGTIPKEIPAWQLHTQPEVEFQVDSPPAPRPSLQPHRLLDHR 360

Qy 361 DSVEQAVLASLGILSLFGLVAGALGLWLRLRRGGKDGSPKPGFLASVIPVDRRPGAP 420
 Db 361 DSVEQAVLASLGILSLFGLVAGALGLWLRLRRGGKDGSPKPGFLASVIPVDRRPGAP 420

Qy 421 NL 422
 Db 421 NL 422

RESULT 4
AAE14613
ID AAE14613 standard; Protein; 422 AA.
XX
AC
XX
XX
DT 18-JUN-2002 (first entry)
XX
DE Human interleukin-11 receptor.
XX
XX Human; interleukin-11; receptor; IL-11R; Immune deficiency;
KW haematopoietic progenitor cell; cancer; bone loss; osteoporosis;
KW Paget's disease; multiple myeloma; hypogonadal condition.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "Putative signal peptide. The specification
FT also refers to alternative signal peptides 1..22 and
FT 1..25"
FT Protein 24..422
FT /note= "Putative mature IL-11 receptor. This region
FT is specifically referred to in claim 1 of the
FT specification. Alternative mature IL-11R proteins
FT 23..422 and 26..422 are also disclosed in the
FT specification"
FT Region 24..324
FT /note= "This region is specifically referred to in
FT claim 1 of the specification"
FT Region 24..345
FT /note= "This region is specifically referred to in
FT claim 1 of the specification"
FT Region 24..359
FT /note= "This region is specifically referred to in
FT claim 1 of the specification"
FT Domain 24..365
FT /label= Extracellular_domain
FT /note= "This region is specifically referred to in claim
FT 1 of the specification. Alternative extracellular domains
FT 23..365 and 26..365 are also disclosed in the
FT specification"
FT Domain 24..111
FT /label= Immunoglobulin_(Ig)-like_domain
FT /note= "Alternative Ig-like domains 23..111 and 26..111
FT are also disclosed in the specification"
FT Domain 112..365
FT /label= Type-I_cytokine_domain
FT /note= "This region is specifically referred to in claim
FT 1 of the specification"
FT Region 112..422
FT /note= "This region is specifically referred to in
FT claim 1 of the specification"
FT Domain 366..390
FT /label= Transmembrane_domain
FT Domain 391..422
FT /label= Intracellular_domain
FT /note= "This region is specifically referred to in claim
FT 1 of the specification"
XX
XX US6350855-B1.
XX
PD 26-FEB-2002.
XX
XX 15-SEP-1997; 97US-0929846.
XX
PR 14-JUN-1996; 96US-0663584.
PR 22-DEC-1994; 94US-0362304.
XX
XX (GEMY) GENETICS INST INC.
XX

PI Tobin J;
XX WPI; 2002-215268/27.
DR N-PSDB; AAD27928.
XX
PT Novel isolated human interleukin-11 receptor protein useful in assays
PT to screen for binding agents and for treating immune deficiencies,
XX cancer and bone related disorders, e.g., osteoporosis.
XX
PS Claim 1; Column 19-22; 20pp; English.
XX
CC The present sequence is human interleukin-11 receptor (IL-11R).
CC IL-11R is involved in the regulation of immune system by interaction
CC with IL-11. The IL-11R polypeptide may be used to screen for agents that
CC bind to it or interfere with the binding of IL-11, as diagnostic agent
CC for detecting the expression or presence of IL-11R, IL-11 or cells
CC expressing IL-11R or IL-11. The IL-11R and IL-11R inhibitors may be
CC useful in treatment or modulation of IL-11-related conditions which
CC include immune deficiencies, specifically deficiencies in haematopoietic
CC progenitor cells, or related disorders, cancer and other diseases.
CC It is also believed that IL-11 and IL-11R may play a role in the
CC regulation of bone maturation and repair. As a result, human IL-11R
CC protein and IL-11R inhibitors may be useful in treatment of bone loss
CC (including that associated with osteoporosis, post-menopausal
CC osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
CC disease, multiple myeloma and hypogonadal conditions).
XX
SQ Sequence 422 AA;
Query Match 100.0%; Score 2275; DB 23; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSCSLSRVLVAVATALVSASSPCQAWGPPGVQVQGPGRSVKLCPCGVTAGDPVSWF 60
DB 1 MSSSCSLSRVLVAVATALVSASSPCQAWGPPGVQVQGPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEPKLLQGPDSGLGHGHELVLAQADSTDEGTYICQTLDGALGGTVTLQLGYPARPVYSC 120
DB 61 RDGEPKLLQGPDSGLGHGHELVLAQADSTDEGTYICQTLDGALGGTVTLQLGYPARPVYSC 120
QY 121 QAADYENFSCWTSPQISGLPTRYLTYSRKTVLGADSQRRSPSTGPPCPQDPLGAARC 180
DB 121 QAADYENFSCWTSPQISGLPTRYLTYSRKTVLGADSQRRSPSTGPPCPQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENVNPLGASTRLLDVLSLOSILRPDPQGLRVESVFGYPRRLRASW 240
DB 181 VVHGAEFWSQYRINVTENVNPLGASTRLLDVLSLOSILRPDPQGLRVESVFGYPRRLRASW 240
QY 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVYASARDFLD 300
DB 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVYASARDFLD 300
QY 301 AGTWSTWSPAWGTPTSTGTTPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQHPRLDHR 360
DB 301 AGTWSTWSPAWGTPTSTGTTPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQHPRLDHR 360
QY 361 DSVEQVAVLASLGLSFLGVAGALALGLWRLRRGKDCSPRPGFLASVIVDVRRCAP 420
DB 361 DSVEQVAVLASLGLSFLGVAGALALGLWRLRRGKDCSPRPGFLASVIVDVRRCAP 420
QY 421 NL 422
DB 421 NL 422
RESULT 5
AAE14613
ID AAE14613 standard; Protein; 423 AA.
XX
AC AAE14613;
XX
XX 21-MAY-1996 (first entry)
DT

XX DE Human interleukin-11 receptor alpha chain.
 XX KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
 XX KW therapy; diagnosis.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..23
 XX FT Protein /label= Sig_peptide
 XX FT Domain /label= Mat_protein
 XX FT Domain /label= Extracellular_domain
 XX FT /note= "the extracellular domain includes
 XX FT haemopoietin and Ig-like domains"
 XX FT Domain 367..392
 XX FT /label= Transmembrane_domain
 XX FT Domain 393..423
 XX FT /label= Cytoplasmic_tail
 XX PN WO9607737-A1.
 XX PD 14-MAR-1996.
 XX PF 05-SEP-1995; 95WO-AU00578.
 XX PR 05-SEP-1994; 94AU-0007902.
 XX PR 05-SEP-1994; 94AU-0007901.
 XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX PI Hilton DJ;
 XX WPI; 1996-171612/17.
 XX DR N-PSDB; AAT17869.
 XX PT Nucleic acid encoding haemopoietin receptor containing conserved
 XX PT amino acid motif esp. IL-11 receptor alpha chain - used for
 XX PT developing IL-11 (ant)agonists
 XX PS Claim 8; Page 47-49; 87pp; English.
 XX CC The human interleukin-11 (IL-11) receptor alpha chain (AAR92814)
 XX CC was identified by expression of DNA (AAT17869) isolated from human
 XX CC bone marrow cDNA libraries. Expression of the human IL-11
 XX CC receptor alpha chain results in specific-binding of human IL-11
 XX CC and permits IL-11 signalling. The receptor alpha chain can be used
 XX CC to develop agonists or antagonists of therapeutic apn. or in
 XX CC the treatment or diagnosis of conditions involving a deficiency of
 XX CC IL-11, excess IL-11 or aberrant effects of normal endogenous IL-11
 XX CC levels.
 XX SQ Sequence 423 AA;
 Query Match 99.2%; Score 2257.5; DB 17; Length 423;
 Best Local Similarity 99.5%; Pred. No. 1.9e-149;
 Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MSSSCGSLRVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 Db 1 MSSSCGSLRVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 QY 61 RDGEPKLLQGPDSGLGHELVLAQAQSTDEGTICQTLGALGGTTLQIGYPPARPVVSC 120
 Db 61 RDGEPKLLQGPDSGLGHELVLAQAQSTDEGTICQTLGALGGTTLQIGYPPARPVVSC 120
 QY 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTIVLGADSORRSPSTGPPCPQDPLGAARC 180
 Db 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTIVLGADSORRSPSTGPPCPQDPLGAARC 180
 QY 181 VVHGAEFWSQYRINTEVNPL-GASTRLLDVSLQSLTRDPDPPQGLRVESVPCYPRGLRAS 239

Db 181 VVHGAEFWSQYRINTEVNPLGASTRLLDVSLQSLTRDPDPPQGLRVESVPCYPRGLRAS 240
 QY 240 WTYPASWPCQPHFLKFRLOYRPAQHPANWSTVEPAGLEEVIITDAVAGLPHAYRVASARDFL 299
 Db 241 WTYPASWPCQPHFLKFRLOYRPAQHPANWSTVEPAGLEEVIITDAVAGLPHAYRVASARDFL 300
 QY 300 DAGTWTSTWSPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVDSPPAPRPSLOPHPRLLDH 359
 Db 301 DAGTWTSTWSPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVDSPPAPRPSLOPHPRLLDH 360
 QY 360 RDSVEQVAVLASLGLSFLGLVAGALALGLWLRRLRRGKDGSPKPGFLASVIPVDRRPGA 419
 Db 361 RDSVEQVAVLASLGLSFLGLVAGALALGLWLRRLRRGKDGSPKPGFLASVIPVDRRPGA 420
 QY 420 PNL 422
 Db 421 PNL 423
 RESULT 6
 AAR92813
 ID AAR92813. standard; Protein; 432 AA.
 XX AC
 XX AAR92813;
 XX DT 21-MAY-1996 (first entry)
 XX DE Murine interleukin-11 receptor alpha chain.
 XX KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
 XX KW therapy; diagnosis.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..23
 XX FT Protein /label= Sig_peptide
 XX FT Domain /label= Mat_protein
 XX FT /label= Extracellular_domain
 XX FT /note= "the extracellular domain includes
 XX FT haemopoietin and Ig-like domains"
 XX FT Domain 368..393
 XX FT /label= Transmembrane_domain
 XX FT Domain 394..432
 XX FT /label= Cytoplasmic_tail
 XX PN WO9607737-A1.
 XX PD 14-MAR-1996.
 XX PF 05-SEP-1995; 95WO-AU00578.
 XX PR 05-SEP-1994; 94AU-0007902.
 XX PR 05-SEP-1994; 94AU-0007901.
 XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX PI Hilton DJ;
 XX WPI; 1996-171612/17.
 XX DR N-PSDB; AAT17868.
 XX PT Nucleic acid encoding haemopoietin receptor containing conserved
 XX PT amino acid motif esp. IL-11 receptor alpha chain - used for
 XX PT developing IL-11 (ant)agonists
 XX PS Claim 6; Page 42-44; 87pp; English.
 XX CC The murine interleukin-11 (IL-11) receptor alpha chain Nr1
 XX CC (AAR92813) was identified by expression of DNA (AAT17868) isolated

CC from adult mouse liver cDNA libraries. Nrl is a low affinity
 CC receptor for IL-11 and interacts with gpl30 to generate a high
 CC affinity IL-11 receptor. IL-11 can be used to develop
 CC agonists or antagonists of therapeutic appln. or in the treatment
 CC of diagnosis of conditions involving a deficiency of IL-11,
 CC excess IL-11 or aberrant effects of normal endogenous IL-11
 CC levels.
 XX
 SQ Sequence 432 AA;

Query Match 83.4%; Score 1897; DB 17; Length 432;
 Best Local Similarity 83.5%; Pred. No. 2.7e-124;
 Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSCSGLRLVAVATLVASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MSSCSGLTRVLVAVATLVSSSPCQAWGPPGVQYQGRVPMVLCPCGVSAGTPVSWF 60

QY 61 RDGEFKLLQGPDSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
 DB 61 RDGSRLLQGPDSGLGHELVLAQVDSDEGTYVCTLDGSGGMVTLKLGPPARPVYSC 120

QY 121 QAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORRSPSTGPPWPCQDPLGAARC 180
 DB 121 QAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORRSPSTGPPWPCQDPLGAARC 180

QY 181 VVHGAEFWSQRYINVTENPLGASTRLDVSILQSLRDPDQGLRVESVPGYPRRLRASW 240
 DB 181 VVHGAEFWSQRYINVTENPLGASTRLDVSILQSLRDPDQGLRVESVPGYPRRLHASW 240

QY 241 TYPASWPCQPHFLKFRQYRPAQHPASTVEPAGLEVIITDAVAGLPHAVRVSARDFLD 300
 DB 241 TYPASWRRQPHFLKFRQYRPAQHPASTVEPAGLEVIITDAVAGLPHAVRVSARDFLD 300

QY 301 AGTWSTWSPWAGTPTGTIPKEIPAWGQLHTQ--PEVEPQVDSFAPPRLPQLPRLLD 358
 DB 301 AGTWSAWEAFWSTPTGTIPKEIPAWGQLHTQ--PEVEPQVDSFAPPRLPQLPRLLD 358

QY 359 HRDSVEQVAVLASGLISFLGLVAGALGLWLRRLRGKDGSPKPGFLASVIVDRLRP 418
 DB 361 HRDPLEQVAVLASGLISFLGLVAGALGLWLRRLRGKDGSPKPGFLASVIVDRLRP 418

QY 419 APNL 422
 DB 421 IPNL 424

RESULT 7
 AAB36653
 ID AAB36653 standard; Protein; 432 AA.
 AC AAB36653;
 AC AAB36653;
 DT 13-MAR-2001 (first entry)
 DE Mouse IL-11 receptor subunit alpha protein SEQ ID NO:10.
 DE
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder.
 OS Mus sp.
 PN WO200073451-A1.
 PD 07-DEC-2000.
 PF 30-MAY-2000; 2000WO-US14867.
 PR 01-JUN-1999; 99US-0322913.
 PA (SCHE) SCHERING CORP.
 XX

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
 DR WPI; 2001-061536/07.
 XX
 PT Novel composition comprising DNAX cytokine receptor subunit polypeptide
 PT useful for regulating immune system function and for treating
 PT immunological disorders -
 XX
 PS Disclosure; Page 13-15; 93pp; English.
 XX
 CC The present invention describes a composition (I) comprising a
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
 CC The DCRS2 polypeptide is useful for binding ligands and for preparing
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for
 CC detecting presence of their ligands and in drug screening assays. It
 CC is also useful for treating conditions such as immunological disorders.
 CC The present sequence represents a cytokine receptor subunit protein
 CC which is given in an alignment of various cytokine receptor subunits in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 432 AA;

Query Match 82.2%; Score 1871; DB 22; Length 432;
 Best Local Similarity 82.5%; Pred. No. 1.8e-122;
 Matches 350; Conservative 19; Mismatches 53; Indels 2; Gaps 1;

QY 1 MSSCSGLRLVAVATLVASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MSSCSGLTRVLVAVATLVSSSPCQAWGPPGVQYQGRVPMVLCPCGVSAGTPVSWF 60

QY 61 RDGEFKLLQGPDSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
 DB 61 RDGSRLLQGPDSGLGHELVLAQVDSDEGTYVCTLDGSGGMVTLKLGPPARPVYSC 120

QY 121 QAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORRSPSTGPPWPCQDPLGAARC 180
 DB 121 QAADYENFSCWSPQISGLPTRYLTYSYRKKTVLGADSORRSPSTGPPWPCQDPLGAARC 180

QY 181 VVHGAEFWSQRYINVTENPLGASTRLDVSILQSLRDPDQGLRVESVPGYPRRLRASW 240
 DB 181 VVHGAEFWSQRYINVTENPLGASTRLDVSILQSLRDPDQGLRVESVPGYPRRLHASW 240

QY 241 TYPASWPCQPHFLKFRQYRPAQHPASTVEPAGLEVIITDAVAGLPHAVRVSARDFLD 300
 DB 241 TYPASWRRQPHFLKFRQYRPAQHPASTVEPAGLEVIITDAVAGLPHAVRVSARDFLD 300

QY 301 AGTWSTWSPWAGTPTGTIPKEIPAWGQLHTQ--PEVEPQVDSFAPPRLPQLPRLLD 358
 DB 301 AGTWSAWEAFWSTPTGTIPKEIPAWGQLHTQ--PEVEPQVDSFAPPRLPQLPRLLD 358

QY 359 HRDSVEQVAVLASGLISFLGLVAGALGLWLRRLRGKDGSPKPGFLASVIVDRLRP 418
 DB 361 HRDPLEQVAVLASGLISFLGLVAGALGLWLRRLRGKDGSPKPGFLASVIVDRLRP 418

QY 419 APNL 422
 DB 421 IPNL 424

RESULT 8
 AAR99091
 ID AAR99091 standard; Protein; 441 AA.
 AC AAR99091;
 AC AAR99091;
 DT 09-OCT-1996 (first entry)
 DE Murine Etl-2 gene product.
 DE
 KW Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
 KW osteoporosis; Paget disease; myeloma; Etl-2.
 XX

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OS Mus sp.
XX W09619574-A1.
XX 27-JUN-1996.
XX 27-NOV-1995; 95WO-US15400.
XX 22-DEC-1994; 94US-0362304.
XX (GEMY ) GENETICS INST INC.
XX Tobin JF;
PI WPI; 1996-309588/31.
DR N-PSDB; AAT32613.
XX New nucleic acid encoding human interleukin 11 receptor - and
PT related protein, antibodies, receptor antagonists, etc, useful for
PT treating and preventing loss of bone mass
XX Example 1; Page 37-40; 54pp; English.
XX The amino acid sequence of the murine Etl-2 gene product is given
CC in AAR99091. Probes based on the Etl-2 gene (AAT32613) were used
CC to screen a human cDNA library, yielding a cDNA clone (AAT33278) that
CC coded for human interleukin-11 receptor (AAR99090), a protein
CC involved in bone maturation and repair.
XX Sequence 441 AA;
SQ
Query Match 80.5%; Score 1831; DB 17; Length 441;
Best Local Similarity 83.1%; Pred. No. 1.le-119;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;
QY 16 ATALVSSSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSGL 75
DB 25 ATALVSSSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSGL 84
QY 76 GHELVLQAQDSTDEGTYICOTLDGALGGTTLQLGYPARPVVSQAADYENFSCWSPS 135
DB 85 GHRVLQAQVDSPEGTYVCQTLDGVSQGMVTLKLGFPVAGTVPVSWFRDGPVKLLQGPDSGL 144
QY 136 QISGLPTRYLTYSRKTKVLGADSQRRSPSTGPPWPCQDPPLGAARCVVHGAEPWSEYRINV 195
DB 145 QVSGLPTRYLTYSRKTKLPGAESQRESPTGPPWPCQDPPLGAARCVVHGAEPWSEYRINV 204
QY 196 TEVNPGLASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
DB 205 TEVNPGLASTCLLDVRLQSLILRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
QY 256 FRLOYRPAQHAWSTVEPAGLEEVITDAVAGLPFAVRVSARDFLDAGTWSTWSPAWGTP 315
DB 265 FRLOYRPAQHAWSTVEPAGLEEVITDAVAGLPFAVRVSARDFLDAGTWSTWSPAWGTP 324
QY 316 STGTPKEIPAWGQLHTQ--PEVEQVDSFAPPSPRSLOPHRLLDHRDSEVQAVLASLG 373
DB 325 STGPLEIDEIPDSQGHQGLEAVAGQESPAFARSLQDPRLDHRDLEQAVLASLG 384
QY 374 ILSFTGLVAGALGLWLRRLRGKDGSPKPGFLASVIVPDRRRGAPNL 422
DB 385 IFSCLGLAVGALGLWLRRLRSRGDKGPKPGILLAPMIPVEXLPGIPNL 433
RESULT 9
AAU007726
ID AAU007726 standard; Protein; 441 AA.
XX
XX AAU007726;
XX
XX 04-DEC-2001 (first entry)
XX
XX Mouse Etl-2.

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XX Mouse; interleukin 11 receptor; IL-11R; cytostatic; antianaemic;
KW osteopathic; leukopaenia; bacterial infection; viral infection; anaemia;
KW B cell deficiency; T cell deficiency; haematopoietic cell deficiency;
KW bone marrow transplantation; immune deficiency; cancer; osteoporosis;
KW Paget's disease; multiple myeloma; hypogonadism; Etl-2.
XX Mus sp.
XX US6274547-B1.
XX 14-AUG-2001.
XX 10-SEP-1998; 98US-0151102.
XX 14-JUN-1996; 96US-0663584.
XX 15-SEP-1997; 97US-0929846.
XX (GEMY ) GENETICS INST INC.
XX Tobin J;
XX WPI; 2001-549157/61.
XX N-PSDB; AAS11971.
XX Binding inhibition of interleukin-11 to the human IL-11 receptor,
PT useful for treatment of anaemia comprises administration of a
PT composition containing a human IL-11R receptor protein comprising
PT specific amino acid sequence -
XX
XX Example 1; Column 26-28; 19pp; English.
XX The invention relates to a method of inhibition binding of interleukin-11
CC (IL-11) to the human IL-11 receptor comprises administration of a
CC composition containing a human IL-11R receptor protein comprising an
CC amino acid sequence of 24-365, 102-365, 24-359, 24-345 or 24-324 amino
CC acids of the human IL-11R protein sequence appearing as AAU07725. The
CC method is used for inhibiting binding of IL-11 to the human IL-11
CC receptor for the treatment of leukopaenia, bacterial and viral
CC infections, anaemia, B cell or T cell deficiencies such as immune cell or
CC haematopoietic cell deficiency followed by bone marrow transplantation,
CC immune deficiency, cancer, regulation of bone maturation and repair, bone
CC loss (including that associated with osteoporosis, post-menopausal
CC osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
CC disease, multiple myeloma and hypogonadal conditions). The present
CC sequence represents mouse Etl-2. The cDNA sequence encoding Etl-2 was
CC used to design probes which were used to isolate the cDNA encoding Human
CC IL-11R
XX
SQ Sequence 441 AA;
Query Match 80.5%; Score 1831; DB 22; Length 441;
Best Local Similarity 83.1%; Pred. No. 1.le-119;
Matches 340; Conservative 17; Mismatches 17; Indels 2; Gaps 1;
QY 16 ATALVSSSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSGL 75
DB 25 ATALVSSSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWFRDGPVKLLQGPDSGL 84
QY 76 GHELVLQAQDSTDEGTYICOTLDGALGGTTLQLGYPARPVVSQAADYENFSCWSPS 135
DB 85 GHRVLQAQVDSPEGTYVCQTLDGVSQGMVTLKLGFPVAGTVPVSWFRDGPVKLLQGPDSGL 144
QY 136 QISGLPTRYLTYSRKTKVLGADSQRRSPSTGPPWPCQDPPLGAARCVVHGAEPWSEYRINV 195
DB 145 QVSGLPTRYLTYSRKTKLPGAESQRESPTGPPWPCQDPPLGAARCVVHGAEPWSEYRINV 204
QY 196 TEVNPGLASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
DB 205 TEVNPGLASTCLLDVRLQSLILRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
QY 256 FRLOYRPAQHAWSTVEPAGLEEVITDAVAGLPFAVRVSARDFLDAGTWSTWSPAWGTP 315
DB 265 FRLOYRPAQHAWSTVEPAGLEEVITDAVAGLPFAVRVSARDFLDAGTWSTWSPAWGTP 315

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Db 265 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWEAWGTP 324
 QY 316 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRRPSLQHPRLLDHRDSVEQVAVLASLG 373
 Db 325 STGPLEQDEIPDWSQGHGQOLEAVVAQEDSPAPARPSLOPDRPLDRDPLEQVAVLASLG 384
 QY 374 ILSFLGLVAGALALGLWLRLRGKDGSPKPGFLASVIPVDRRPGAPNL 422
 Db 385 IFSCGLGAVGALALGLWLRLRRSGDKGPKGLLAPMIPVEKLPGLP 433

RESULT 10
 AAEL14614
 ID AAEL14614 standard; Protein; 441 AA.
 XX
 AC AAEL14614;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Murine Etl-2 protein.
 XX
 KW Murine; Etl-2; interleukin-11 receptor; IL-11R; immune deficiency;
 KW haematopoietic progenitor cell; cancer; bone loss; osteoporosis;
 KW Paget's disease; multiple myeloma; hypogonadal condition.
 OS Mus sp.
 XX
 PN US6350855-B1.
 XX
 PD 26-FEB-2002.
 XX
 PF 15-SEP-1997; 97US-0929846.
 XX
 PR 14-JUN-1996; 96US-0663584.
 PR 22-DEC-1994; 94US-0362304.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Tobin J;
 XX
 DR WPI; 2002-215268/27.
 DR N-PSDB; AAD27929.
 XX
 PT Novel isolated human interleukin-11 receptor protein useful in assays
 PT to screen for binding agents and for treating immune deficiencies,
 PT cancer and bone related disorders, e.g., osteoporosis -
 XX
 PS Disclosure; Column 25-28; 20pp; English.
 XX
 CC The invention relates to human interleukin-11 receptor (IL-11R). The
 CC IL-11R is involved in the regulation of immune system by interaction
 CC with IL-11. The IL-11R polypeptide may be used to screen for agents that
 CC bind to it or interfere with the binding of IL-11, as diagnostic agent
 CC for detecting the expression or presence of IL-11R, IL-11 or cells
 CC expressing IL-11R or IL-11. The IL-11R and IL-11R inhibitors may be
 CC useful in treatment or modulation of IL-11-related conditions which
 CC include immune deficiencies, specifically deficiencies in haematopoietic
 CC progenitor cells, or related disorders, cancer and other diseases.
 CC It is also believed that IL-11 and IL-11R may play a role in the
 CC regulation of bone maturation and repair. As a result, human IL-11R
 CC protein and IL-11R inhibitors may be useful in treatment of bone loss
 CC (including that associated with osteoporosis, post-menopausal
 CC osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
 CC disease, multiple myeloma and hypogonadal conditions). The present
 CC sequence is murine Etl-2, used to illustrate the invention.
 XX
 SQ Sequence 441 AA;

Query Match 80.5%; Score 1831; DB 23; Length 441;
 Best Local Similarity 83.1%; Pred. No. 1.le-119;
 Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;
 QY 16 ATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSVFRDGPRLKLGPDGSL 75

Db 25 ATALVSSSSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSVFRDGPRLKLGPDGSL 84
 QY 76 GHELVLQAQADSTDEGTYYICQTLDDGALGGVNTLQLGYPARPVYVSCQAADYENFSCWTSPS 135
 Db 85 GHRLVLAQVDSDEGTYYVCQTLDDGSGGMVTLKLGFPARPVEVSCQADYENFSCWTSPG 144
 QY 136 QISGLPTRYLTYSRKKTVLGADSQRRSPSTGPPCPQDPLGAARCWVHGAETWSOYRINV 195
 Db 145 QVSGLPTRYLTYSRKKTLPGAESQRESPTGPPCPQDPLEASRCVWHAETWSEYRINV 204
 QY 196 TEVNPLGASTRLLDVLSLILRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
 Db 205 TEVNPLGASTCLLDVRLQSLILRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
 QY 256 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWEAWGTP 315
 Db 265 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWEAWGTP 324
 QY 316 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRRPSLQHPRLLDHRDSVEQVAVLASLG 373
 Db 325 STGPLEQDEIPDWSQGHGQOLEAVVAQEDSPAPARPSLOPDRPLDRDPLEQVAVLASLG 384
 QY 374 ILSFLGLVAGALALGLWLRLRGKDGSPKPGFLASVIPVDRRPGAPNL 422
 Db 385 IFSCGLGAVGALALGLWLRLRRSGDKGPKGLLAPMIPVEKLPGLP 433

RESULT 11
 AAY59390
 ID AAY59390 standard; Protein; 379 AA.
 XX
 AC AAY59390;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Murine soluble interleukin-11 receptor.
 XX
 KW Interleukin-11; IL-11; IL-11R; human; bone density disorder; gp130;
 KW IL-11 tertiary complex; glycoprotein 130; postmenopausal bone loss;
 KW bone resorption inhibitor; bone formation; therapy.
 XX
 OS Mus sp.
 XX
 PN WO99595608-A2.
 XX
 PD 25-NOV-1999.
 XX
 PF 19-MAY-1999; 99WO-CA00516.
 XX
 PR 19-MAY-1998; 98CA-2237915.
 XX
 PA (HAMI-) HAMILTON CIVIC HOSPITAL RES DEV CORP.
 XX
 PI Shaughnessy S, Austin RC;
 XX
 DR WPI; 2000-062377/05.
 DR N-PSDB; AAZ40400.
 XX
 PT Inhibiting formation of a tertiary complex for the treatment of
 PT osteoporosis -
 XX
 PS Example 3; Page 46-50; 61pp; English.
 XX
 CC This sequence is the soluble mouse interleukin-11 receptor (IL-11R).
 CC The invention relates to a method of treating or alleviating the symptoms
 CC of a pathological condition in which bone density is decreased comprises
 CC inhibiting the formation of a tertiary complex of IL-11, IL-11 receptor
 CC and glycoprotein 130 (gp130) in a mammalian patient suffering from such a
 CC condition. The method is used to treat or alleviate the symptoms of a
 CC pathological condition in which bone density is decreased, especially
 CC postmenopausal bone loss. The IL-11 binding peptide is useful in the
 CC purification of IL-11 or in depleting IL-11 from a solution. TRAP

CC (tartrate-resistant acid phosphatase) and bone marrow formation assays
 CC can be used for the identification of IL-11 antagonists. The method not
 CC only inhibits bone resorption and hence bone loss, but also increases the
 CC process of bone formation to increase bone density.

XX Sequence 379 AA;

Query Match 73.8%; Score 1680; DB 21; Length 379;
 Best Local Similarity 84.2%; Pred. No. 3.1e-109;
 Matches 310; Conservative 17; Mismatches 39; Indels 2; Gaps 1;

QY 1 MSSSCGSLRVLVAVATLVASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MSSSCGSLRVLVAVATLVASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 QY 61 RDGEPKLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVWSC 120
 DB 61 RDGSRLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGSGGMVTLKLGFPARPVWSC 120
 QY 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGWPCCQDPPLGAARC 180
 DB 121 QAVDYENFSCWSPSQISGLPTRYLTSYRKKTLPGAESQRESPTGWPCCQDPPLGAARC 180
 QY 181 VHGAEFWSEYRINVTENPLGASTCLLDVRLQSLRDPDPQGLRVESVPSYPRRLHASW 240
 DB 181 VHGAEFWSEYRINVTENPLGASTCLLDVRLQSLRDPDPQGLRVESVPSYPRRLHASW 240
 QY 241 TYPASWPCQPHFLKFRLOYRPAQHPANSTVEPAGLEIVITDAVAGLHAYRVASRDFLD 300
 DB 241 TYPASWPCQPHFLKFRLOYRPAQHPANSTVEPAGLEIVITDAVAGLHAYRVASRDFLD 300
 QY 301 AGTWSPEAWGTSTGTIPKEIPAWGQLHTQ--PEVEPOVDSAPPSPSLQHPRLLD 358
 DB 301 AGTWSPEAWGTSTGTIPKEIPAWGQLHTQ--PEVEPOVDSAPPSPSLQHPRLLD 358
 QY 359 HRDSVEQV 366
 DB 361 HRDPLEQL 368

RESULT 12

ID ABB06126 standard; Protein; 257 AA.

XX ABB06126;

DT 10-MAY-2002 (first entry)

XX Human NS protein sequence SEQ ID NO:218.

XX Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotrophic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antidiabetic; immunomodulator; cardiac;
 KW anticonvulsant; antidiabetic; tranquiliser; antidepressant; neuroleptic;
 KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW infertility; cardiovascular disease; coagulation disease; hypertension;
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.

XX Homo sapiens.

OS WO200206315-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-IL00653.

XX

PR 18-JUL-2000; 2000IL-0137345.

PR 15-DEC-2000; 2000IL-0140354.

XX (COMP-) COMPUGEN LTD.

XX Mintz L, Freilich S, Bernstein J;

XX WPI: 2002-155037/20.

DR N-PSDB; ABL39780.

XX One hundred and twenty eight novel nucleic acid sequences, useful for
 treating and diagnosing e.g. cancer, asthma and Alzheimer's -

PS Claim 6; Page 254-255; 290pp; English.

XX ABL3991 to ABL39818 represent novel human nucleic acid sequences
 encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
 vasotrophic, antiarteriosclerotic, antiinflammatory, dermatological,
 anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
 anticoagulant, antifibrinolytic, hypotension, antidiabetic, cardiant,
 immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antiulcer,
 antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
 nootropic and contraceptive activities. The NS can be used in vaccines,
 gene therapy and antisense therapy. Nucleic acids, expression vectors and
 antibodies from the present invention can be used for treating and
 diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 disease, coagulation disease, ischaemia, hypertension, asthma, immune
 depression, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 depression, schizophrenia, viral disease, gastric ulcers, stroke,
 Alzheimer's disease and as a contraceptive.

SQ Sequence 257 AA;

Query Match 33.9%; Score 771; DB 23; Length 257;

Best Local Similarity 61.5%; Pred. No. 4.8e-46;

Matches 160; Conservative 14; Mismatches 42; Indels 44; Gaps 6;

QY 51 VTAGDP-VSWFRDGEPLKLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALG-----GT 104

DB 1 MASGVPELSGVGDGCELVRSRPGYGH-----SAAGITEDEQQLRAQGGPGRGYSPGV 56

QY 105 VTQLQ-----GYPPARPVWSCQAADYENFSCWSPSQI 137

DB 57 CLLPLPGLGPRGPVWAARQVREAVLSWSDCRDPARPVWSCQAADYENFSCWSPSQI 116

QY 138 SGLPTRYLTSYRKKTVLGADSQRRSPSTGWPCCQDPPLGAARCVVHGAEFWSEYRINVT 197

DB 117 SGLPTRYLTSYRKKTVLGADSQRRSPSTGWPCCQDPPLGAARCVVHGAEFWSEYRINVT 176

QY 198 VNPLGASTRLDVSLSQSLRDPDPQGLRVESVPGVPRRLRASWTYPASWPCP-----HF 252

DB 177 VNPLGASTRLDVSLSQSLRDPDPQGLRVESVPGVPRRLRASWTYPASWPCP-----HF 252

QY 253 LLKFRLOYRPAQHPAWSTVE 272

DB 237 CSTVRSRIQPG--PRWSQLD 254

RESULT 13

AAAR22616

ID AAR22616 standard; Protein; 460 AA.

XX AAR22616;

XX 04-NOV-1992 (first entry)

XX IL-6R for soluble IL-6R prodn.

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